

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 12

TO: Jennifer Graser

Location: REM/3B09/3C18

Art Unit: 1645 June <u>7</u>, 2004

Case Serial Number: 10/712713

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

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                                                                                           (without alignments)
5417.965 Million cell updates/sec
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Compugen Ltd
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US-08-936-165A-179
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US-09-265-417-61
US-09-528-709-61
US-09-527-745-61
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 GenCore version (c) 1993 - 2004
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                                                      OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                      Gapop_60.0 , Gapext 60.0
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seq length: 2000000000
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Match Length DB
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                                                                                                                                                 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
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FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: P8248P1
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFCATION: «Unknown»
PRIOR APPLICATION DATA:
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Pred. No. 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 392:
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TELEPHONE: (240) 314-1224
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100.0%; Pre
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LENGTH: 2424 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 392:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                       SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                       ZIP: 20850
COMPUTER READABLE FORM
ADDRESSEE: Human
STREET: 9410 Key
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                                          CITY: Rockville
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Matches 1314;
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Best Local Similarity 99.7%; Pred. No. 1.1e-119;
Matches 325; Conservative 0; Mismatches 1;
                                                                          CITY: King of Prussia COUNTY: King of Prussia STATE: PA
COUNTY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 950549
TELECOMMUNICATION INFORMATION:
                                         Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021 CAACCACACTTTCTCTAGAACACA 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 619 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-936-165A-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 610-270-4478
  534
                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 610-270-5090
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  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1527 GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                   GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAIGTTACAAATATTAAAAGAAGCATTAGAAACGTTTGGTGGTGATAAACGTCGTTTCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTATTGGGTGCAGGTGATATT
                                                               GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT
                                                                                                                                                AFTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT
                                                                                                                                                                                                                                   TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACCACACATTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGTAGCGTTTTAA 1940
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; Sequence 179, Application US/08936165A
; Patent No. 6348582
                     1107
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Gaps

840 552

492 900

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COMPUTER READBLE FORM:

ZIP: 90071-2066

COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: BEOCRAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFTCATION: 435
PRIOR APPLICATION ATA: 1995
APPLICATION NUMBER: 60/009,102
FILING DATE: September 12, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELECOMMUNICATION NUMBER: 240/247
TELECOMMUNICATION NUMBER: 240/247
TELECOMMUNICATION NUMBER: 240/247
TELECOMMUNICATION NUMBER: 240/247
                    CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6.
SEQUENCE CHARACTERISTICS:
LENGTH: 888 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
     NUMBER OF SECUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-09-265-315-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-265-315-61/c
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STREET: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
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| Patent No. 6187541
| GENERAL INFORMATION:
| APPLICANT: Beaton, Bret
| APPLICANT: Mation, Prancois
| APPLICANT: Mation, Patrick K. |
| APPLICANT: Schmid, Molly B. |
| APPLICANT: Schmid, Molly B. |
| TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS |
| TITLE OF INVENTION: TARGET GENES |
| TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 888;
APPLICANT: Malouin, Francois
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
APPLICANT: Sum, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.8%; Score 90; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 8.6e-33;
Matches 90; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1209 ATTAGAACAATTTGATAATGCTGTTATTTT 1238
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                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZIP: 90071-2066
COUNTRY: BADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPACIBLE
COMPUTER: IBM COMPACIBLE
COMPUTER: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPRENCE/CDOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                 ADDRESSE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 888 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-714-918-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
TELEX: 6'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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0; Gaps
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| Patent No. 6187541 | Patent No. 6187541 |
| APPLICANT Bencon, Bret APPLICANT Bencon, Bret APPLICANT Bencon, Prancois APPLICANT Schmid, Molly B. APPLICANT Schmid, Molly B. APPLICANT Schmid, Molly B. TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS TITLE OF INVENTION: TARGET GENES NUMBER OF SEQUENCES: 111
| CORRESPONDENCE ADDRESS: 111
Length 888;
                                                        Indela
  Query Match 6.8%; Score 90; DB 3; Le Best Local Similarity 100.0%; Pred. No. 8.6e-33; Matches 90; Conservative 0; Mismatches 0;
                                                                                                                                                                                                           1209 ATTAGAACAATTTGATAATGCTGTTATTTT 1238
                                                                                                                                                                                                                                                             507 ATTAGAACAATTTGATAATGCTGTTATTTT 478
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; TOPOLOGY: linear
US-09-266-417-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1. Application US/09266417

Patent No. 622858

GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Benton, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 90; DB 3; L
100.0%; Pred. No. 8.6e-33;
tive 0; Mismatches 0;
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                                                                                                                                                        MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: MARCH 9, 1999
CLASSIFICATION: 435
FILING DATE: September 13, 1996
APPLICATION NUMBER: 06/1009,102
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 32,327
REFERENCY/PORCY NUMBER: 32,327
REFERENCY/PORCY NUMBER: 32,327
REFERENCY/PORCY NUMBER: 240/247
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEPTEMBER: 240/247
TELECOMUNICATION SEQ ID NO: 61:
INFORMATION FOR SEQ ID NO: 61:
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 888 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100. Matches 90; Conservative
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-09-265-315-61
                                                                  RY: U.S.A.
90071-2066
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                       CITY: LOS
STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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APPLICANT: Benton, Bret
Lee, Ving
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
Sun, Dongxu
TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
6.8%; Score 90; DB 3; Length 888;
Best Local Similarity 100.0%; Pred. No. 8.6e-33;
Matches 90; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1209 ATTAGAACAATTTGATAATGCTGTTATTTT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: 1BM Compatible
COMPUTER: 1BM Compatible
COMPUTER: 1BM Compatible
COMPUTER: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CUASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: September 12, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 20,03,398
FILING DATE: NUMBER: 240/248
TELECOMMUNICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STRERT: 633 West Fifth Street
Sulte 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-528-709-61/c
; Sequence 61, Application US/09528709
; Patent No. 6630303
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 888 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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Search completed: June 6, 2004, 07:10:16
Job time : 136 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Leus
o. 8.6e-33;
0;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                    ATTORNAY JOACH
ATTORNAY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32.327
REFERENCE/DOCKET NUMBER: 222/005
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELERAX: (213) 955-0440
TELERAX: (7-3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERSTICS:
LENGTH 888 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1209 ATTAGAACAATTTGATAATGCTGTTATTTT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/527,745
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,709
FILING DATE: 17-Mar-2000
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507 Arragaacaarrrcaraarccrcrrarrr 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.8%; Score 90; DB Best Local Similarity 100.0%; Pred. No. 8.6 Matches 90; Conservative 0; Mismatches
                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1596
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 61, Application US/09527745
Patent No. 6638718
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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0; Gaps
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100.0%; Pred. No. 8.6e-33;
tive 0; Mismatches 0; Indels
                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WAIDING, RICHARD J. REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1209 ATTAGAACAATTTGATAATGCTGTTATTTT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          507 ATTAGAACAATTTGATAATGCTGTTATTTT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 61:
FILING DATE: 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 888 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.C
Matches 90; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

Run on:

OM nucleic - nucleic search, using sw model

June 6, 2004, 04:34:41; Search time 315 Seconds (without alignments) 5591.218 Million cell updates/sec

US-10-712-713-1 1318 1 atgacacactatcattttgt......gaaaaatgcgttttaagctt 1318

Title: Perfect score: Sequence:

OLIGO_NUC Gapop_60.0 , Gapext 60.0 Scoring table:

2089662 seqs, 668146292 residues

Searched:

20 Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Pending Patents NA New:*

1: /cgn2 6/ptcdata/2/pna/DSO NEW COMB.seq:*

2: /cgn2 6/ptcdata/2/pna/USO6 NEW COMB.seq:*

3: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:*

4: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:*

5: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:*

5: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:*

7: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:*

7: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:* 128.432....7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match Length DB

Result

Description

No matches found

Search completed: June 6, 2004, 08:36:08 Job time: 315 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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June Run on:

OM nucleic - nucleic search, using sw model

US-10-712-713-1 1318 Title: Perfect score:

1 atgacacactatcattttgt......gaaaaatgcgttttaagctt 1318 Sequence:

OLIGO_NUC Gapop_60.0 , Gapext 60.0 Scoring table:

27513289 seqs, 14931090276 residues Searched:

20 Word size :

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match Length DB

Result

Description

No matches found

Search completed: June 6, 2004, 07:07:51 Job time: 3824 secs

OM nucleic

on:

Run

Sequence:

Searched:

Database

No.

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Result

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BX415878 BX415878
BX437758
BX437758
BX437758
BX437675
BX45609 BX45675
BX45609 BXTFW53TF
BJ376728 BJ376728
BJ376728 BJ376728
BJ376728 BJ376728
BJ376728 BJ376728
BJ376728 BJ376728
BJ37697 BJ376728
BJ313987 Danio rer
AZ55026 ENTEVSBTR
BX13987 BJ37697
BX43979 BX437697
BX43979 BX437758
BX43979 BX437758
BJ330059 BJ330059
BHJ78274 DIL © 05
AL615231 T7 end of
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LLMGtag738 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
BH771016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domaine de Vilvert, 78352 Jouy en Josas cedex, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 2937)
Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments (2002) In press
Contact: Sorokin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAJ INRA, Domaine de Vilvert, 78352 Jouy en J.
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Fax11: Sorokine@jouy.inra.fr
best homologue in strain IL1403 is murC (91$)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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High quality sequence start: 30
High quality sequence stop: 2907,
    BX415878

BX43758

CNS 005EVL

AZ548467

AZ548467

AZ5484609

BJJ 76728

BJJ 76728

BX415058

BX439120

BX139987

AZ55026

BX415878

BX439779

BX439779

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BX13059

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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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           00000000
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BH384961 AG-ND-161
BH400896 AG-ND-145
AL063921 Drosophil
                                                                                                                                                                                              (without alignments)
10292.457 Million cell updates/sec
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                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                          27513289 seqs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
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GSS 01-MAY-2002

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TTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGGTGTTAAAACGTCGTTTCAATGAAA
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/clone lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                  /sub species="cremoris"
/db xref="taxon:1359"
/clone lib="WG1363 Random Sequence Tag Library"
/note="Vector: pSGW15 Site 1: Smal; Library of
chromosomal fragments of L.Tactis strain MG1363 was
prepared by partial Alul digestion or by sonication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 373.6; DB 28; Length 2937;
Pred. No. 4e-68;
0; Mismatches 454; Indels 5;
                                                                                                    'organiem="Lactococcus lactis subep. cremoris"
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/strain="MG1363"
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Best Local Similarity 59.4;
Matches 671; Conservative
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Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 3543
Email: bloftuegetigur.org
Email: bloftuegetigur.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae BEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&W University BAC Center
University, College Station, Texas 17843-2123, USA using a Hindill
partial digest.
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Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J., Ren, C., Huff, B.R., Carlile, J.L., Black, K., Zhang, H.-B., Gardher, M.J. and Collins, F.H. Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African
                                                                                                                                                                                                                                                                                                                                       CTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTTCAAC
                                                                                 905 CTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATTAGTG
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Anopheles gambiae
Eukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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Query Match
Best Local
Matches 183
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Hong, Y. S., Hogan, J. R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,
Ren, C., Huff, B.R., Carlile, J.L., Black, K., Zhang, H.-B.,
Gardner, M.J. and Collins, F.H.
Construction of a BAC library and generation of BAC end
sequence-tagged connectors for genome sequencing of the African
malaria mosquito Anopheles gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003)
                                                                                                              624 GGAGCAAGCTATGAAGATCTTAAAAAAAGGAATTAAATCTTTCAAAGGGATTAAAAGAAG
                                                                         834 GAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCG
                                                                                                                                                  TTTCAATGAAACTACAATTGCAAAT---CAAGTTATTGTAGATGATTATGCACACCATCC
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
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 Length 728;
Score 90; DB 28; Length 72
Pred. No. 1.1e-08;
0; Mismatches 215; Indel8
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The Institute for Genomic Research
Tylz Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
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Anopheles gambiae
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Contact: Brendan J Loftus
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   Query Match 6.8%;
Best Local Similarity 51.6%;
Matches 232; Conservative
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to minimize the inclusion of DNA from microorganisms that inhabit the DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
Seq primer: M13 For Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 TATTAGATATATATCCAGCTCGTGAATTGCCAATAGAAGGTGTGACTTCTGATTGGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        920 AAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATTAGTGCTACAATTGAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 TARARACCTTTTATCCCGATARARGCTGTTARTAGTCTTTCAACCGCATTTATTTACCA
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                     Location/Qualifiers
1. 584
1. 0584
2. organism="Anopheles gambiae"
/mol type="genomic DNA"
/strain="PEST"
/db xref="taxon:7165"
/clone="AG-ND-145A13"
/clone_lib="ND-TAM"
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/note="Vector: pCMVSPORT 6, 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                                                                                                                       EST 15-MAY-2003
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                                                                                                                          BX415878 115-MAY-2003
BX415878 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008Y104
                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1200)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 192 91006 EVRY cedex - France
BP 193 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : filang@lifetech.com URL
http://fulliangfh.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP008BE02QF1.
Location/Qualifiers
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440 TITWIWITWWAATIAITITWITWTAAAAAAAWWWWWWTWIAIAI 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"

/mol_type="mRNA"
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/clone="CSGAP00819104"
/tissuc_type="THYMUS"
/clone_lib="Homo sapiens_THYMUS"
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BX415878
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                       melanogaster genome using these BACB. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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          The BDGP is constructing a physical map of the Drosophila
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/mol type="genomic DNA"
/db Xref="taxon:7227"
/clone="BACR08K:0"
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17.7%; Pred. No. 5.7e-07
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/note="end : TET3"
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/clone_lib="Homo saphens THYMUS"
/clone_lib="Homo saphens THYMUS"
/note="Wector: pcMvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMvSPORT 6 vector. Library was not normalized."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP008CA01QP1.
                                                                                                                                                                                                                                                                                                                                                <u>CAATGAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGA</u>
                                                                                                TATITITITIMAATITIWAATIWITITITIMAWAATAAAAATAWAAAAAAAATIWIWMAA
                                                                                                                                                                                                     1017 ATTTCAACCACACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTT
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP008YB01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-PRIME, mRNA Bequence.
BX437758
BX437758.1 GI:30773605
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RESULT

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Gaps

16;

Length IndelB

Query Match 5.9%; Score 77.8; DB 13; Best Local Similarity 31.6%; Pred. No. 3.9e-06; Matches 272; Conservative 169; Mismatches 404;

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1014
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                                                                                                                                                                                                                               :: | | | | : : | | : : TWARAAAAAWWIWWWAARGRARGTITTTTTTAAWWGGGAGRIAWWIWITWTTTTTTTT
TWARAAAAAAAWWIWWWAARGRARGTITTTTTTTAAWWGGGAGRIAWWIWITWTTTTTTTT
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                                            505 ACAAATATTGATTTCGATCATCCTGATTATTTTTAAAGATATTAATGATGTTTTTTGATGCA
                                                                 GGTGAGTTTTTATGATCACTTCCTGTCTCCACAATATGGTGACCATACAGTTTTAAATGCA
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                                                                                                                                                                                                                                                                                        TICCAAGAAATGGCACATAAAAAAAGGTATTATTGCTTGGGGTGATGATGAACAT
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
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/db xref="taxon:5759"
/db xref="taxon:5759"
/clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Textamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, LiS. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Waking small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                GSS 14-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library Seg primer: M13-Reverse
                                                                                                                                                                                             AZ548467 908 bp DNA linear GSS 14-NOV-20
ENTEK30TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                          Entamoeba histolytica

Bukaryota, Entamoebidae, Entamoeba.

1 (bases 1 to 908)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 9543
Email: bjloftus@tigr.org
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                                                                                                                                                                                                                                                         Genomic, genomic survey sequence.
AZ548467
AZ548467.1 GI:11172102
                                 991 ATTWWIAWTAWATATTTATTAA 1015
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/strain="HM1:IMSS"
1290 ATTAGGCATGAAAAATGCGTTTTAA 1314
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High quality sequence stop: 828.
Location/Qualifiers
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Matches 363; Conserv
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   ਨੇ
                                                                                                         Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
Bp 191 91006 ENYEY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr
- Web : www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Gosegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RRCI-98 and was constructed by patfial
ECORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="teaxon:7227"
/clone="BACR29B23"
/clone_lib="RPCI-98"
/note="end: T7"
                                                                                          Genoscope
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organism="Homo sapiens" mol_type="mRNA" db_xref="taxon:9606"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1206 IGTATTAGAACAATTIGATAATGCTGTTATTITATTTATGGGTGCAGGTGATATTCAAAA 1265
                                                                                                                                                                                                                                                                                                                                                                                                                             966 TACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTTCAACC 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1026 ACACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGTAAAGC 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1145 HORATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCATTAAC
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1099 bp mRNA linear EST 22-MAY-2003

BX456575 Homo sapiens THYMUS Homo sapiens cDNA clone CSUCAP002YD04
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213 TGATGATGAAGATGATGAAGACGATGAAGACGACGAATATGAATTAGAAGATGATGATGA
                                                                                                               TITIGATGIGIATGIGGATGGTGAGITITIATGATCACTICCTGTCTCCACAATAIGGTGA 785
                                                                                                                                                     393 TGATGAAGATGATGAAGACGATGAAGACGACGAATATGAATTAGAAGATGATGAAGA 452
                                                                                                                                                                                                                                                                         846 TACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAATGAAAC 905
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Catarrhini; Hominidae; Homo.
                                                                           CCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTAGATGT
                                                                                                                                                                                                                                                                                                           813 TGATGAAGATGATGAAGATGATGAAGACGACGAATTTTGAATTTAAAGATGAGATGATGATGAAA
                                       ATTTAAAGATTCGGATGACATTTATGCTCAAATATTCAAATTACGGATAAAGGTACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 19106 ENRY cedex - France
Libral: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com Uhttp://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP002D802QPL.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Verte
Mammalia, Eutheria, Primates, Catarrhini, Hor
1 (bases 1 to 1099)
Lil,W.B., Gruber,C., Jessee,J. and Polayes,D.
Inll-length cDNA libraries and normalization
Unpublished (2001)
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BX456575
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DEFINITION
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TITLE
JOURNAL
COMMENT
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/clone="CSOCARD002YD04"
/tissue type="THYMUS"
/clone_lb="Howers type="THYMUS"
/clone_lb="Howers type="THYMUS"
/note="Vector: pcWVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned it the Not I and EcoRV sites of the pcMVSPORT 6 vector. Library was not normalized."
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Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 849)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKKRGTKKDKRDAKKKGGARAKKKGRAWKTKKKGAAARRAAWAARWAAAAAAAATATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTTTTTGATGTGTATGTGGTGATGTTTTTATGATCACTTCCTGTCTCCAATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    618 ATKTKTTTTTGAWTGAATWTTTTTATTAATGTTTTGTTGGTTADAWAWTTTGTAAWATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 TACTICAGIAGCIGIAACIGGIGCACAIGGIAAAACTICIACAACAGGIITAITAICACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGATTTAAAGATTCGCATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 678 AAAAATGGRATTTGAAAAAKRGAAWGGRAWWAAAATTKGTTTAAATTGAAAATGAAT
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                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                         Query Match 5.4%; Score 71.8; DB 13; Length 1099; Best Local Similarity 26.6%; Pred. No. 7.2e-05; Matches 157; Conservative 169; Mismatches 263; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTAGA
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AZ546009
AZ546009.1 GI:11167130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 TAATAAGAAATTTAATAAGAAATTAGATATTACAGGTAGTGATGAAGAATATGATGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 GACAAATATTGGATTTTCGATCATCCTGATTATTTTAAAGATATTAATGATGTTTTTTGATGC 563
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BJ376728 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc29013 3', mRNA sequence.
                                                                                                                                                                                                                                                                                  Dictyostelium discoideum
Dictyostelium discoideum
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (Dases 1 to 754)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               572 TGBAGGAGAGAAAAGBAATCAAAAGAAATGGATGAAGAATTTGATAAAATGTTAAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Tal: Nishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69.6; DB 12;
Pred. No. 0.00021;
0; Mismatches 285;
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/clone="ddc29013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                               BJ376728.1 GI:19286111
EST.
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1000 AAAGAAGTIGTIGCAG
                                         91 GATGAAGATGATGAAG
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Best Local Similarity 46.8
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2002)
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                                                                                                          RESULT 11
BJ376728/c
                                                                                                                                                                          DEFINITION
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  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Entamoba histolytica Sheared DNA"
/clone lib="Entamoba histolytica Sheared DNA"
/note="Vector: pHOS1; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, WD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotque sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
DNA 11: brait derived from the Entamoeba histolytica HM1:IMSS sheared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCATCCTGATTATTTTAAAGATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGATGTTCCAATTTATTATGGATTTAAAGATTCGGATGACATTTATGCTCAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 TTTGAATTAGAAGATGAAGAAGATGAAGATGATGATGAAGACGAAGAAGACGAAGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATAATGTTAAAAAAGGTATTATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70.4; DB 28; Length 849;
Pred. No. 0.00014;
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                                                                                                                                                                                                                                                                                                                                                                                organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                      High quality sequence start: 26
High quality sequence stop: 796.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db xref="taxon:5759"
    HM1:IMSS sheared DNA library
                    Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                             Seq primer: M13-Forward
Class: shotgun
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ilarity 46.4%;
Conservative
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Contact: L. David Sibley
WashU Plasmodium EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA sequencing by:
Washington University Genome Sequencing Center For information on obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco
High quality sequence stop; 422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 bp mRNA linear EST 11-SEP-2002 PERSToab93a09.yl Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum 3D7 cDNA Fishilar to TR:096253 096253 HYPOTHETICAL 220.3 KD PROTEIN.;, mRNA sequence.
                                                                                                                                                                                                     1108 AFTTTTGGATCAATTAGAGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAA 1167
                                                                                                                                                                                                                                                                                                                                          1168 ATTGAAGGTGCATCGTTAATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAAT 1227
                                                                                                                                                                                                                                                                       477
                                                                                                                                                                                                                                                                                                                                                                                                          417
656 AAAAAMAYATHTATAWAAAATATWTWAAWAAWAAWAAAAAAAAACATWTTWCAAAAWTTWT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang.K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D., Marra,M., Hiller,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,E., Ronko,I., Taagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Waterston,R., Wilson,R. and Sibley,D. Franklin,C., Levinso,D., Waterston,R., Wilson,R. and Sibley,D.
                                                                      GCATTTTTAAATGAATTTGCAGAAAGTTTAAGTAAAGCAGATCGTGTATTCTTATGTGAA
                                                                                                                                  536 TITITITITITATAIAMMMMHWAAIWTITITTAWATIWTWAIAAAAAWTITITITT
                                                                                                                                                                                                                                                                                                                                                                                 1228 GCTGTTATTTTATTTATGGGTGCAGGTGATATTCAAAAATTACAAAATGCATAT 1281
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Plasmodium falciparum 3D7"
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BU498120
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KEYWORDS
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/tissue type="THYMUS"
/clone_lib=#Homo saplens THYMUS"
/note="Vector: pCWVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and scloned into Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                           1056 bp mRNA linear BST 15-MAY-2003
3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAATTGCGATTAGTTATTTAGAGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAA 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  871 ACGTTTGGTGGTGTTAAACGTCGTTTCAATGAAACTACAATTGCAAATCAAGTTATTGTA 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            931 GATGATTATGCACACCATCCAAGAGAAATTAGTGCTACAATTGAAACAGCACGAAA---G 987
                                                                                                      TGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTAGATGTTACAAATATTAAAGA 860
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1056)
                                                                                                                                                                     TGAAAGTGAATTAGAAGAAATTAAAGATTTCCATAGGATAAAAAAGGGCAAGATCTTAGN 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invirrogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invirrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAFO004AblONPl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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/db_xref="taxon:9606"
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AL536104 1inear EST 31-MAY-2003 AL536104 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF022XC18 5-PRIME, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
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Contact: Genoscope

Control National de Sequencage

BP 191 91006 EVRY cedex - France

BR 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

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(Stratagene), the phagemids were preciptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
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On Feb 13, 2001 this sequence version replaced gi:12799597.
                                                                                                                                                                                                                                           Score 68.2; DB 13; Length 594;
Pred. No. 0.00042;
0; Mismatches 238; Indels 0
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Best Local Similarity 47.0%;
Matches 211; Conservative (
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Danio rerio genomic clone DKEY-99E7, genomic survey sequence.

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         /dev_grege="fetal"
/dlone_lib="fetal"
/clone_lib="fetal"
/note="forgan brain, Vector: pCMVSPORT 6, 1st strand cDNA
/note="forgan: brain, Vector: pCMVSPORT 6, 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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(Dases 1 to 844)

Humphray, S. J., Huckle, E. and Durham, J. L.
                                                                                                                                                                                                   875 TTGGTGGTGTTAAACGTCGTTTCAATGAAACTACAATTGCAAATCAAGTTATTGTAGATG
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                                                                                                                           Ouery Match 5.1%; Score 67.8; DB 9; Length 1201; Best Local Similarity 32.1%; Pred. No. 0.00049; Matches 195; Conservative 112; Mismatches 298; Indels 3
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Direct Submission
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: This sequence was generated from the T7 end of BAC 9987. 9987 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:

Acygene. Further details:

http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                                                                                                                                                                                                                                           /organism="Danio rerio"
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      TITLE
JOURNAL
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Length 844; ORIGIN

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486 ACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTTAAAGATAT 545

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546 TAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATTATTGC 605

ITGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTATTATGG 665 909

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666 ATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGTACTGC 725

Search completed: June 6, 2004, 02:44:40 Job time : 3829 secs

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5.1.6
Compugen Ltd.
  GenCore version (c) 1993 - 2004
            Copyright
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- protein search, using sw model OM protein Run on:

June 3, 2004, 14:32:30 ; Search time 59 Seconds (without alignments) 2092.767 Million cell updates/8ec

US-10-712-713-2 score: Perfect Title:

1 MTHYHFVGIKGSGMSSLAQI......GDIQKLQNAYLDKLGMKNAF 437

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	Description	Aau00828 S. aureus	Abm71210 Staphyloc	Add15465 Staphyloc	Add15463 Staphyloc	Abul5856 Protein e	Aau33801 Staphyloc	Aau36700 Staphyloc	Aaw87771 UDP-N-ace	Abp40288 Staphyloc	Abu43254 Protein e	Abu18407 Protein e	Abu29382 Protein e	Aau35277 Enterococ	Abu29727 Protein e	Abb48762 Listeria	Abu33064 Protein e	Adb11616 Alloiococ	Abb55394 Lactococc	Abp27818 Streptoco			Abu44255 Protein e	Aau37914 Streptoco	Abu46149 Protein e	Abu01979 S. pneumo
	ID	AAU00828	ABM71210	ADD15465	ADD15463	ABU15856	AAU33801	AAU36700	AAW87771	ABP40288	ABU43254	ABU18407	ABU29382	AAU35277	ABU29727	ABB48762	ABU33064	ADB11616	ABB55394	ABP27818	ABP27819	ABU46471	ABU44255	AAU37914	ABU46149	ABU01979
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*	Query Match	100.0	100.0	100.0	100.0	100.0	9.66	9.66	98.4	87.3	87.3	64.6	63.2	63.0	61.4	59.0	59.0	57.1	51.9	51.1	50.1	50.1	49.8	49.2	49.2	49.1
	Score	2275	2275	2275	2275	2274	2267	2267	2238	1986	1985	1470	1438.5	1433.5	1396	1342	1342	1298.5	1180	1163.5	1139	1139	1132.5	1119	1119	1117
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Aaw89199 Partial s	Abu43391 Protein e	Aaw55120 Streptoco	Abp54614 S. pneumo	Adc45197 S. pneumo	Adc97287 E. faeciu	Abu24704 Protein e	Abu23758 Protein e	Abu25700 Protein e		Ada33736 Acinetoba	Abu33503 Protein e	Aay74419 Neisseria		Abu37200 Protein e	Aay74417 Neisseria	Abp80545 N. gonorr	Abu19357 Protein e	Aay74418 Neisseria	Abu35149 Protein e
AAW89199	ABU43391	AAW55120	ABP54614	ADC45197	ADC97287	ABU24704	ABU23758	ABU25700	ABU16741	ADA33736	ABU33503	AAY74419	ABU38136	ABU37200	AAY74417	ABP80545	ABU19357	AAY74418	ABU35149
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215	246	422	422	422	291	461	458	450	482	492	469	506	506	469	506	506	468	506	486
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1067	1064	1043	1043	1043	967	690.5	641.5	585.5	574	574	559	548	548	545	545	545	538	535	532
56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 AAU00828

AAU00828 standard; protein; 437 AA

AAU00828;

(first entry) 04-JUL-2001 S. aureus UDP-N-acetylmuramate:L-alanine ligase, MurC.

UDP-N-acetylmuxamate:L-alanine ligase; MurC; immunogen; vaccine; antibody; wound infection; cellulitis; burn infection; eyelid infection; food poisoning; joint infection; neonatal conjunctivitis; esteomyelitis; skin infection; scalded skin ayudrome; toxic epidermal necrosis; Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis.

Staphylococcus aureus.

137. .139 // label = Antigenic_epitope 236. .239 /label= Antigenic_epitope Location/Qualifiers Key Region Region

WO200116292-A2.

08-MAR-2001.

31-AUG-2000; 2000WO-US023773. 99US-0151933P. 01-SEP-1999;

(HUMA-) HUMAN GENOME SCI INC.

Choi GH;

WPI; 2001-183259/18. N-PSDB; AAS00189 New isolated nucleic acid for use in diagnosing Staphylococcus infections and in vaccines for eliciting immune responses to the infections.

Claim 9; Page 14; 225pp; English.

The sequence represents S. aureus Murc (UDP-N-acetylmuramate:L-alanine ligase). The polynucleotides of the invention are used to detect Staphylococcus nucleic acids in a biological sample from an animal for diagnosing Staphylococcus infections. The polypeptides of the invention

27-MAR-2001; 2001GB-00007661

(CHIR-) CHIRON SPA

from an animal to diagnose Staphylococcus infections. The polypeptides are also used in vaccines to elicit protective antibodies in an animal to a member of the Staphylococcus genues and for preventing or attenuating an infection caused by a member of the Staphylococcus genus e.g wound infection, cellulitis, burn infection, eyelid infection, food poisoning, joint infection, meonatal conjunctivitis, osteowyellitis, bkin infection, escaled skin syndrome (also known as toxic epidermal necrosis, Ritter's disease and izyell's disease), toxic shock syndrome and endocarditis. The polymucleotides may also be used in vaccines and for preventing or attenuating a Staphylococcus infection. Antibodies to the polypeptides may be used to purify, detect and target the polypeptides in in vitro and in vivo diagnostic and therapeutic methods used to detect anti-Staphylococcus antibodies in a biological sample

Sequence 437 AA;

ö 241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALBFRGGVKRRFN 300 360 240 300 361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI 420 DMVVIQGNAFASSHEEIVRAHQIKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120 180 121 HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 180 240 9 ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS 61 DMVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRFFN DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG **ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS** 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE 121 HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYALMTNIDFDHPDYFK Gaps ; 0 Length 437; Indels 100.0%; Score 2275; DB 4; 100.0%; Pred. No. 9.7e-193; ô 0; Mismatches OKLONAYLDKLGMKNAF 437 QKLQNAYLDKLGMKNAF Conservative Query Match Best Local Similarity Matches 437; Conserv 61 361 181 301 301 421 421 d ð 셤 g ò 음 ਨੇ g à 셤 à 엄 유 ò à

RESULT 2 ABM71210 à

ABM71210 standard; protein; 444 AA. (first entry) 20-NOV-2003

Staphylococcus aureus protein #450.

gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target Antibacterial; vaccine;

Staphylococcus aureus

444 AA.

standard; protein;

ADD15465

15-JAN-2004 (first entry)

ADD15465;

XXXE

28-NOV-2002

27-MAR-2002; 2002WO-IB002637.

240 187 The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis. DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 188 DINDVPDAFQEMAHNVKKGIIAMGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 248 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE 61 DMVVIQGNAFASSHERIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 68 DMVVIQGNAFASSHEBIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK **ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS** ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI Gaps ; 0 Length 444; Indels Query Match
100.0%; Score 2275; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.9e-193;
Matches 437; Conservative 0; Mismatches 0: Claim 1; SEQ ID NO 900; 49pp; English. Σ Scarselli OKLONAYLDKLGMKNAF 437 OKLONAYLDKLGMKNAF Masignani V, Mora M, 2003-120786/11. N-PSDB; ACF72770 Sequence 444 AA; 301 368 121 181 241 308 361 421 RESULT 3 ADD15465 XXCCCCCCCXXXIIIXXXXXXCCCCCCXXXX 셤 g 유 유 à à 셤 ò 셤 ਨੇ ₽ ઠે ਨੇ ₽

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immunological response; vaccination; shrface disinfectant;
personal hygiene application; food preservative; enzyme; MurC;
UDP-N-acetylmuramate-alanine ligase. microbial; antimicrobial; membrane biopynthesis; pathogenic; Staphylococcus aureus MurC protein (SeqID 30) 20-SEP-2002; 2002WO-CA001428 Staphylococcus aureus. WO2003025007-A2. 18-DEC-2001;

2001US-0324152P. 2001US-0324692P. 2001US-0341732P. 2001US-0323992P 2001US-0341776P 19-DEC-2001; 2001US-0341949P 21-SEP-2001; 25-SEP-2001; 18-DEC-2001; 21-SEP-2001;

Vedadi M, Alam MZ, Awrey D, Beattie B; Kanagarajah D, Nethery K, Ng I, Mansoury K; Viola C, Wrezel O; (AFFI-) AFFINIUM PHARM INC. Dharamsi A, Houston S, Pinder B, V Edwards A, Domagala M, Mcdonald M,

WPI; 2003-468119/44. N-PSDB; ADD15464. Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria.

Claim 20; SEQ ID NO 30; 325pp; English.

developing antimicrobial agents for use as surface disinfectants, personal hygiene applications and as food preservatives or in treating food products to eliminate potential pathogens. This polypeptide sequence is the Murc protein encoded by experimentally predicted DNA from S. aureus UDP-N-acetylmuramate-alanine ligase of the invention. information to aid the discovery of therapeutic molecules to treat disorders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for species This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus), Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli) that provide novel antimicrobial targets. Specifically, it refers to polypeptides that are involved in membrane biosynthesis, which play a critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate characterisation by labelling with isotopic or heavy atoms, and also thus microbial species of fusion proteins.

Sequence 444 AA;

ö Gaps o, Length 444; Indels Score 2275; DB 7; Pred. No. 9.9e-193; 0; Mismatches 0; Query Match
Best Local Similarity 100.0%;
Matches 437; Conservative 0;

- 9 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE
- 67 MTHYHFVGIKGSCMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE

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61 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120

300 180 240 360 127 187 247 307 367 420 427 HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK TAFDVYVDGEFYDHFLSPQYGDHTVLANLAVIAISYLEKLDVTNIKEALETFGGVKRRFN HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK DINDVFDAFQEMAHNVKKGIIAMGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN **ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVRQPHTFSRTQAFLNEFAESLS ETTIANQVIVDOYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS** 368 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINRDSINVLEQFDNAVILFMGAGDI 437 QKLQNAYLDKLGMKNAP **QKLQNAYLDKLGMKNAF** 248 308 428 68 121 128 181 188 241 301 361 421 ò 셤 à 셤 ð 셤 à 요 à 임 Š

RESULT 4 ADD15463

ADD15463 standard; protein; 444 AA.

ADD15463;

(first entry) 15-JAN-2004 Staphylococcus aureus MurC protein (SeqID 28).

microbial; antimicrobial; membrane biosynthesis; pathogenic; immunological response; vaccination; surface disinfectant; personal hygiene application; food preservative; enzyme; MurC; UDP-N-acetylmuramate alanine ligase.

Staphylococcus aureus

WO2003025007-A2.

20-SEP-2002; 2002WO-CA001428 27-MAR-2003

2001US-0324152P 2001US-0323992P 2001US-0339924P 2001US-0350973P 2001US-0340924P 29-OCT-2001; 30-OCT-2001; 27-NOV-2001; 21-SEP-2001; 25-SEP-2001; 26-OCT-2001; 21-SEP-2001;

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2001US-0333666P, 2001US-0341732P, 2001US-0341776P 2001US-0341949P 18-DEC-2001; 19-DEC-2001;

(AFFI-) AFFINIUM PHARM INC.



Ϋ, Beattie B; I, Mansoury Vedadi M, Alam MZ, Awrey D, Kanagarajah D, Nethery K, Ng Viola C, Wrezel O; Dharamei A, Houeton S, Pinder B, V Domagala M, Mcdonald M, Edwards A,

2003-468119/44. N-PSDB; ADD15462.

Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in

This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus), Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli) that provide novel antimicrobial targets. Specifically, it refers to polypeptides that are involved in membrane biosynthesis, which play a critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate characterisation by labelling with isotopic or heavy atoms, and also funion proteins. These proteins provide structural and functional information to aid the discovery of therapeutic molecules to treat disconders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for developing antimicrobial agents for use as surface disinfectants, personal hygiene applications and as food preservatives or in treating food products to eliminate potential pathogens. This polypeptide sequence is the MurC protein encoded by DNA predicted from the genomic sequence S. aureus UDP-N-acetylmuranate-alanine ligase of the invention. membrane biosynthesis, useful as targets for pathogenic bacteria Claim 20; SEQ ID NO 28; 325pp; English

Sequence 444 AA;

ö Gaps .; 0 DB 7; Length 444; Indels Query Match 100.0%; Score 2275; DB 7; Best Local Similarity 100.0%; Pred. No. 9.9e-193; Matches 437; Conservative 0; Mismatches 0;

120 9 67 DMVVIQGNAFASSHERIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE œ 61

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ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS 308 301

367

KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI 427 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI 368 361

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g ò RESULT 5 **ABU15856** ABU15856;

ABU15856 standard; protein; 437 AA.

(first entry) 19-JUN-2003

XXXXXXXX

Protein encoded by Prokaryotic essential gene #1383.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Staphylococcus aureus WO200277183-A2

03-OCT-2002

21-MAR-2002; 2002WO-US009107

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00472851. 06-MAR-2002; 2002US-0362699P

(ELIT-) ELITRA PHARM INC.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, ijά Wang Wall

2003-029926/02 N-PSDB; ACA19726

acreening New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 43780; 1766pp; English.

the nucleic acid inhibits proliferation of a cell. Also included are:

the 6213 antisense sequences given in the specification where expression

of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

encoding a polypeptide whose expression is inhibited by the antisense

muleic acid; (2) a host cell containing the vector; (3) an isolated

conflicted or its fragment whose expression is inhibited by the

antisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide or its fragment whose expression is inhibited by the

conflicteration or the activity of a gene in an operon required for

proliferation or the activity of a gene in an operon required for

the gene product or that has an activity against a biological pathway

conflicted for proliferation, or that inhibits cellular proliferation; (8)

dentifying a gene required for cellular proliferation or the biological

pathway in which a proliferation-required gene or its gene product lies

cor a gene on which the test compound that inhibits proliferation of an

organism acts; (9) manufacturing an antibiotic; (10) profiling a

compound; a activity; (11) a culture comprising strains in which the gene

product is overexpressed or underexpressed; (12) determining the extent

compounds; or (13) identifying the target of a compound that inhibits the

conflicted of the strains is present in a culture or collection of

strains; or (13) identifying the target of a compound that inhibits the

conflicted or of an organism. The antisense nucleic acids are useful for

dentifying proteins or screening for homologous nucleic acids required

conflicted to the strains of the strains in a condident or an underexpiration or the solate enabledence moleic acids required

conditional proliferation of solate condidents for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression ftp.wipo.int/pub/published_pct_sequences

Sequence 437 AA;

Gaps .. 0 Length 437; IndelB DB 6; Pred. No. 1.2e-192 Score 2274; 100.0%; 99.8%; Conservative Best Local Similarity Matches 436; Query Match

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9 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE

9 1 MIHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE

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61 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120

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; antibiotic;

Trawick JD,

Wall D,

development. The antisement of the control of the c themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococous aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterocococus facelis. The invention is also useful for the identification of potential new targets for antibiotic 180 360 360 420 241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 300 121 HVMNGDKKTSFLIGDGTGRGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE 1 MIHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFGANNIKE DMVVIQGNAPASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 181 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKOSDDIYAQNIQITDKG TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKL,DVTNIKEALETFGGVKRRFN **ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVPQPHTFSRTQAFLNEFAESLS ETTIANQVIVDDYAHHPREISATIETARKKYPHKBVVAVFQPHTFSRTQAFLNEFAESLS** DINDVFDAFQEMAHNVKKGIIAMGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVVLFMGAGDI KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI Сарв prokaryotic cellular proliferation protein; antibiotic; ö 4; Length 437; Staphylococcus aureus cellular proliferation protein #870 Indele Score 2267; DB 4; I Pred. No. 5e-192; 1; Mismatches 1; Ä AAU36700 standard; protein; 444 437 OKLONAYLDKLGMKNAF 437 Query Match
Best Local Similarity 99.5%;
Matches 435; Conservative QXC,QNAYLDKC,GMKNAF antibacterial; drug design (first entry) Staphylococcus aureus. Sequence 437 AA; WO200170955-A2 14-FEB-2002 27-SEP-2001 Antisense; 61 19 AAU36700; 121 241 301 361 361 421 181 301 421 AAU36700 q ਨੇ 셤 à 셤 à å ò ઠે g ð g ò 윰 à 셤 300 300 360 420 420 240 240 360 Carr GJ;

240 240 300

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes theore their use in the discovery of novel antibiotics, the essential genes the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebbiela pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins con the used to screen compounds in rational drug discovery programmes. The antisense mucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The presents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in the way intropublished_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS
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                                                                                                                                                                                                                              Trawick JD, Carr GJ;
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                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.6%; Score 2267; DB 4; 99.5%; Pred. No. 5.1e-192; ive 1; Mismatches 1;
                                                                                                                                                                                                                              Wall D,
                                                                                                                                                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 12293; 511pp; English.
                                                                                                                                                                                                                            Zyskind JW,
                                                                2000US-0206848P.
2000US-0207727P.
2000US-0242578P.
2000US-0253625P.
2000US-0253625P.
                                                  2000US-0191078P.
                21-MAR-2001; 2001WO-US009180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.5
Matches 435; Conservative
                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                              Ohlsen KL,
                                                                                                                                                                                                                                                                                  WPI; 2001-611495/70.
N-PSDB; AASS4559.
                                                                                                                                                                                                                                                 Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 444 AA;
                                                                                                                    27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
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Yamamoto RT,
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The present sequence represents a UDP-N-acetylmuramate:L-alanine ligase

(Murc polypeptide) encoded by the S. aureus Murc gene. Host cells

containing an expression system comprising the Murc gene can be used for

the recombinant production of the polypeptide. Agonists or the Murc

copyleptide are used to treat conditions requiring increased activity or

expression of the polypeptide. Antagonists, inhibitory nucleic acid or

competitive polypeptide are useful for inhibiting the polypeptide e.g.

Competitive polypeptide are useful for inhibiting the polypeptide e.g.

Competitive polypeptide are useful for inhibiting they are also useful against

Competitial agents are useful to treat in-dwelling devices for

infection prevention or generally as wound treatments to prevent adhesion

of bacteria to matrix proteins. The Murc polypeptide is also useful for

diagnosing or prognosing a (susceptibility to) disease, for raising

contibodies; to identify modulators or specific receptors; in rational

drug design and as an immunogen for vaccines. The Murc gene sequences are

consetul in antisense/ribozyme therapeutics; to detect mutant Murc gene;

contibodies are immunogen for vaccines. The Murc gene sequences

contibodies are immunogen for vaccines. The Murc gene sequences are

contibodies are immunogen for vaccines. The Murc gene sequences are

contibodies are immunogen for vaccines and for genetic immunications.
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Murc gene; UDP-N-acetylmuramate:L-alanine ligase; Murc polypeptide; bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine; immunogen; drug; genetic immunisation.
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                                                                                                                                                                                                                                                                                                                                            UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide).
                                                                                                                                                                                                                          AAW87771 standard; protein; 437 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 4; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              open reading frame; ORF; bacterial infection;
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                                                       DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS
                                                                                                           HVWNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK
                                                                                                                                                               DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
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DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
                                         DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 5133; 267pp; English.
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gene therapy
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antibacterial;
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08-NOV-1997;
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particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycl or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense, prokaryotic essential gene, cell proliferation, drug design.
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                                                                                       87.3%; Score 1986; DB 5; Length 4
84.7%; Pred. No. 4e-167;
ive 43; Mismatches 24; Indels
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25-OCT-2001; 2001US-0342923P.
PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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les 370; Conserv
                                                                  Sequence 442 AA;
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Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD,

WPI; 2003-029926/02 N-PSDB; ACA47124 antisense nucleic acids, useful for identifying proteins or screening required for cellular proliferation to isolate candidate molecules for rational drug discovery programs homologous nucleic acids

Claim 25; SEQ ID NO 71178; 1766pp; English.

The invention relates to an isolated muteric actu compitating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway or the proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an corganism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibite the proliferation of an organism. The antisense nucleic acids required for cellular proliferations or screening for homologous nucleic acids required for electron or for correspondent and determined acids are useful for for electron or for a compound acids are useful for for electron or for a conditional acids are useful for for electron or an organism. The antisense mucleic acids required for electron or an organism to solate candidate molecules for acquired acids are useful for an account of the strains or screening for homologous nucleic acids required for a solate account of an organism to solate candidate molecules or screening for accou drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the brained from int/pub/published_pct_sequences invention relates to an isolated nucleic acid comprising any one of

Sequence 437 AA;

ö 1 MIHYHFVGIKGSGMSSLAQIMHDLGHBVQGSDIENYVFTEVALRNKGIKILPFDANNIKE Gaps ö 87.3%; Score 1985; DB 6; Length 437; 84.7%; Pred. No. 4.9e-167; Indele 24; ; Pred. No. 4.9e-167; 43; Mismatches 24; Matches 370; Conservative Best Local Similarity Query Match ਨੇ

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Antisense; prokaryotic essential gene; cell proliferation; drug design. Zyskind JW; Xu HH; 361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI Ohlsen KL, Forsyth RA, Protein encoded by Prokaryotic essential gene #3934. Haselbeck R, Yamamoto R, ABU18407 standard; protein; 436 AA. Malone C, Carr GJ, 437 437 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107. 21-MAR-2001; 2001US-00815242. 421 OKLONAYLDKLGMKNAF 421 QKLLKAYFEKLGVKNDF (first entry) (ELIT-) ELITRA PHARM INC. Zamudio C, Trawick JD, WPI; 2003-029926/02. Bacillus anthracis. N-PSDB; ACA22277 WO200277183-A2 19-JUN-2003 03-OCT-2002 ABU18407; Wang L, Wall D, q 셤 à

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

claim 25; SEQ ID NO 46331; 1766pp; English.

the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

Co (i) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated continued acid; (2) a host cell containing the vector; (3) an isolated continued continued in antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation of the pathway in which a proliferation for cellular proliferation of the product lies or a gene on which the test compound that inhibits proliferation of an compound's activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound's activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required in a cidentifying acids required for homologous nucleic acids required for identifying the target of a compound that inhibits the contains. invention relates to an isolated nucleic acid comprising any one of

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for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous mucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent din not form part of the printed specification, but was obtained in electronic format directly from WiPO at the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                          HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DINDVFDAFQEMAHNVKKGIIAMGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #14909
                                                                                                                                                                                                                                  93;
                                                                                                                                                                                            Query Match
64.64; Score 1470; DB 6;
Best Local Similarity 64.74; Pred. No. 2.1e-121;
Matches 279; Conservative 59; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU29382 standard; protein; 445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKLQNAYLDKL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || : ||: ::
OKFEAAYVKEV
                                                                                                                                                            Sequence 436 AA;
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06-SEP-2001; 2
25-OCT-2001; 2
08-FEB-2002; 2
06-MAR-2002; 2
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The invention fracters to an interest actu compilating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a propose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular or the activity of a gene in an operon required for proliferation or that activity of a gene in an operon required for the gene product or that has an activity against a biological pathway or the appropriate for cellular proliferation or the biological pathway or a gene or which the test compound that inhibite proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the gene compound that inhibite proliferation of an organism. The antisense uncleic acids are useful for the which each of the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for deach all manufacturing or homologous nucleic acids required for encounted acids are useful for deach all and acceptance or the strains or the strains or the strains or the strains of the strains or servening for homologous nucleic acids required for deach all and acceptance or the strains of the strains or the strain
                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETT 303
                                                                                                                                                                                                                                                                                                                                                                                   one of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 NGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVPDAPQEMAHNVKKGI LAMGDDEHLRKI BADVPIYYYGPKDSDDIYAQNIQITDKGTAF
                                                               Zyskind Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                     Äξ
                                                                  Ohlsen Forsyth
                                                                     Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 57306; 1766pp; English.
                                                                     Malone C,
Carr GJ,
                     ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 259; Conservative
                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                 2003-029926/02
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                                                                                                                                                                            N-PSDB; ACA33252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 445 AA;
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                     (ELIT-)
                                                                       Wang L,
Wall D,
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240

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Gaps ; 0

Length 436; Indels 300

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes them the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, conserly for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify antibodies capable of binding to the express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The present cands sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in celectronic format directly from WIPO at the printed sequences.
363
                 309 VSDMIIVDDYAHHPAEIKATIDGARQKYPDKEIIAVFQPHTFTRTIALMDEFABALDLAD 368
                                                                                         Carr GJ;
304 IANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKAD
                                                                      364 RVFLCEIFGSIRENTGALTIQDLIDKIE-GASLINEDSINVLEQFDNAVILFMGAGDIQK
                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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antibiotics, comprise sequences of antisense nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis cellular proliferation protein #564.
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                                                                                                                                                                                                                                                                             AAU35277 standard; protein; 456 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2000; 2000US-0191078P.
25-MAY-2000; 2000US-0206848P.
25-MAY-2000; 2000US-020727P.
23-OCT-2000; 2000US-0242578P.
22-DEC-2000; 200US-0253625P.
22-DEC-2000; 200US-02531P.
16-FEB-2001; 200UUS-0269308P.
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Xu HH;
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Yamamoto RT,
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                                                                                                            369 ]
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AAU35277
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123

63 79

Gaps

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DB 4; Length 456; Indels

63.0%; Score 1433.5; DB 4; 60.7%; Pred. No. 3.9e-118; ive 79; Mismatches 87;

Query Match Best Local Similarity 60.74 Matches 258; Conservative

Sequence 456 AA;

X S

199

124 NGDKKTSFLIGDGTGMGLPESDYFAPEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDIN 183

184 DVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGTAF

200

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64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM

4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV

380 EVFLCNIFGSARETQGEVRIEDLGEKIQKGGQVITEDNVSPLLDFENAEVVFMGAGDVQK 439

à g

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364 RVFLCEIFGSIRENTGALTIQDLIDKIE-GASLINEDSINVLEQFDNAVILFMGAGDIQK

320 VSDMIIVDDYAHHPABIKATIDGARQKYPDKEIIAVPQPHTFTRTIALMDEFAEALDLAD

304 IANQVIVDDYAHHPREISATIETARKKYPHKEVVAVEQPHTESRTQAFLNEFAESLSKAD

DVYHKADFVGHFVIPARGHHVIMNALGVIAVAYFEKIDMQKVABEMISFKGVKRRFSEKK 319

244 DVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETT 303

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design.
                                                                                                                                                                                                                                                                           Zyskind JW;
Xu HH;
                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug
                                                                                                                                                                                                                                                                            Ohlsen KL,
Forsyth RA,
                                                                           Protein encoded by Prokaryotic essential gene #15254
                                                                                                                                                                                                                                                                           Haselbeck R,
Yamamoto R,
                  ABU29727 standard; protein; 444 AA.
                                                                                                                                                                                                                                                                             Malone C,
Carr GJ,
                                                                                                                                                                                             21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                            21-MAR-2002; 2002WO-US009107
                                                        19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                             Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                         WPI; 2003-029926/02.
N-PSDB; ACA33597.
                                                                                                                                     WO200277183-A2.
                                                                                                                                                         03-OCT-2002
                                                                                                                                                                                                                                                                              Wang L,
Wall D,
RESULT 14
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us-10-712-713-2.rag

New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs. New antisense nucleic acids, for homologous nucleic acids

Claim 25; SEQ ID NO 57651; 1766pp; English.

the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
confine and inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
concling a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
contisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide of its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide (5) producing the polypeptide; (6) inhibiting cellular
contisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide (5) producing the polypeptide; (6) inhibiting cellular
controliferation, (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
controliferation, (7) identifying a compound that inhibits proliferation of an
configuration agene required for cellular proliferation of an
configuration agene required for cellular proliferation of an
configuration and proliferation—required gene or its gene product lies
or or a gene on which the test compound that inhibits proliferation of
compound's activity; (1) a culture comprising strains in which the gene
confount is overexpressed or undersexpressed; (12) determining the extent
compound's activity; (1) a culture compound that inhibits the
compound that inhibits for
compounds or strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
configuration of an organism. The autisense nucleic acids required
configuration of an organism. The acid model of acid or actional ac drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at The invention relates to an isolated nucleic acid comprising any one of tp.wipo.int/pub/published_pct_sequences

Sequence 444 AA;

123 68 IIAGNAFPDSHEEIQRAKELGLEVIRYHDFIGHFIQNYTSIAVTGSHGKTSTTGLLSHVL 127 63 67 8 YHFVGIKGSGMSSLALVLHEQGLNVQGSDIEKYFFTQRDLEKANITILPFNADNVKPGMT 64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDPLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM 4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV Gaps 5 Length 444; 93; Indels 61.4%; Score 1396; DB 6; 60.6%; Pred. No. 7.9e-115; ive 74; Mismatches 93; Query Match Best Local Similarity 60.6* Matches 260; Conservative g a ð ð ð

> d à d ò a

: || :|| 428 FEQAY-EKL 435 423 LQNAYLDKL 431 à g

screening

ABB48762

ABB48762 standard; protein; 447 AA.

(first entry) 05-FEB-2002

Listeria monocytogenes protein #1466

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.

Listeria monocytogenes

WO200177335-A2

18-OCT-2001.

11-APR-2001; 2001WO-FR001118.

11-APR-2000; 2000FR-00004629.

(INSP) INST PASTEUR.

Dehoux P; Cossart P; Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart E Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Voss H; Кове М,

WPI; 2002-010914/01.

Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.

Claim 6; SEQ ID NO 1467; 192pp; French.

The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained the characteristic formed directive formed formed formed for the formed formed formed formed formed for formed ftp.wipo.int/pub/published_pct_sequences

Sequence 447 AA;

. 0 Length 447; Indels 59.0%; Score 1342; DB 5; 1 59.7%; Pred. No. 4.9e-110; tive 64; Mismatches 108; Matches 255; Conservative Local Similarity Query Match

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1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE 60

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364 RVFLCEIFGSIRENTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDIQK 422

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181 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 240
                                                                   241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 300
                                                                                                        241 TKFDVYHREEFLSSFEIPAYGDHNVLNALSVIALCDYEGLPVEDVKNELKTFEGVKRRFS 300
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Sequence 21952, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 446, App
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6914, App
5023, Ap
2712, Ap
241280, A
6951, Ap
4942, Ap
2891, Ap
5705, Ap
3, Appli
4, Appli
                                                                                                                 June 3, 2004, 14:37:01; Search time 22 Seconds (without alignments) 1025.480 Million cell updates/sec
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/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptcdata/2/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-941-083-116

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US-09-107-532A-6914

US-09-107-532A-6914

US-09-540-039A-12280

US-09-540-039A-24196

US-09-543-681A-6951

US-09-543-681A-6951

US-09-543-681A-6951

US-09-540-236-2891

US-09-540-236-2891

US-09-540-236-2891

US-09-540-236-2891

US-09-540-236-2891

US-09-543-681A-5705

US-09-134-001C-388

US-09-134-001C-388

US-09-134-001C-388

US-09-134-001C-388

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US-09-510-888-2
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US-09-147-928-2
US-09-134-001C-4284
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-08-934-481-2
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                                                                                                                                                                                                                                                                                                                                                     389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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115.5 7.7 455 4 US-09-107-532A-522B Sequence 522B, App 164.5 7.2 452 4 US-09-530-836-6 Sequence 6, Application 7.0 335 3 US-08-961-083-110 Sequence 110, Application 7.0 335 4 US-09-536-784-110 Sequence 110, Application 7.0 451 4 US-09-536-784-110 Sequence 110, Application 7.0 451 4 US-09-144-918-5 Sequence 2, Application 7.0 483 4 US-09-144-918-5 Sequence 2, Application 7.0 483 4 US-09-144-918-5 Sequence 2, Application 7.0 483 4 US-09-489-039A-1236 Sequence 12376, Application 7.0 419 4 US-09-489-039A-12376 Sequence 12376, Application 7.0 419 4 US-09-384-618-4 Sequence 3139, Application 7.0 4 US-09-328-352-6020 Sequence 6020, Application 7.0 4 US-09-343-61A-7027 Sequence 7.027, Application 7.0 4 US-09-104-26-253 Sequence 7.0 4 US-09-104-26-253 Sequence 7.0 4 US-09-1139-5 Sequence 2, Application 7.0 4 US-09-113-954-2 Sequence 2, Application 7.0 4 US-09-113-954-2 Sequence 2, Application 7.0 4 US-09-1143-954-2 Sequence 2, Application 7.0 4 US-09-1143-954-2 Sequence 2, Application 7.0 4 US-09-1143-954-2 Sequence 2, Application 6, Application 7.0 4 US-09-1143-954-2 Sequence 2, Application 6, Applic	1513. Applications and applications are investigated by the property of the principal	Match 87.3%; Score 1986; DB 4; Length 442; ocal Similarity 84.7%; Pred. No. 1.1e-185; indels 0; Gaps 0; ss 370; Conservative 43; Mismatches 24; Indels 0; Gaps 0;	1 MTHYHFVGIKGSGMSSIAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE 60	61 DMVVIQGNAPASSHERIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120 	1 HVMRGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 1	181 DINDVFDAFVERMAHNYKKGILAMGDDEHLKKIEADVFIYYYGFKUSDDIYAQNIQITUKG 240 18
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TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN

ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS

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183 NDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFK-DSDDIYAQNIQITDKGT 241
                                                                                                                                                                      242 AFDVYVDGEFYDHFLSPQYGDHTVLNALAVIALSYLEKLDVTNIKEALETFGGVKRRFNE 301
                                                                                                                                                                                                                                                                 302 ITIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSK 361
                                                                                                                                                                                                                                                                                           305 KIVNDIVIIDDFAHHPTBIIATLDAARQKYPSKEIVAVFQPHFFRTIALLDDFAHAINQ 364
                                                                                                                                                                                                                                                                                                                                                                                   185 EDVFNAFNDYAKQITKGLFVYGEDAELRKITSDAPIYYYGFEAEGNDFVASDLLRSTTGS
                                                                                                                                                                                                   245 TFTVHERGONLGOPHIPTFGRHNIWNATAVIGLLYTAGFDLNLVREHLKTFAGVKRRFTE
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Patent No. 6159469

GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
45.8%; Score 1043; DB 3; Length 422;
Best Local Similarity 48.8%; Pred. No. 1.7e-93;
Matches 200; Conservative 80; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20850
CXMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECHONNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 422 amino acids
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425 IQTYEYSF 432
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STRANDEDNESS: si
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361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI 420
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                            366 KADQVFLCEIFGSIRENIGDLITIEDLINRIDGSTLIDENSIDVLEKFDNAVILFMGAGDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
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7e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 49.2%; Score 1119; DB 4; Length 44
Best Local Similarity 49.8%; Pred. No. 7e-101;
Matches 213; Conservative 84; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,572
                                                                                                                                                                                                                                                                                                                       APPLICANT: Wallis, Nicola G.
APPLICANT: Black, Michael T.
APPLICANT: Black, Michael T.
APPLICANT: Knowles, David J.
APPLICANT: Lonetto, Michael A.
APPLICANT: Nicholas, Robert K.
TITLE OF INVENTION: No. 6310193el Murc
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024022
FILING DATE: 16-AUG-1996
APPLICATION NUMBER: US 08/889711
FILING DATE: 104-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dickingon, Q. Todd
REGISTRATION NUMBER: 28, 3554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P50533-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2252
                                                                                                                                                                                                                                                Sequence 2, Application US/08940572
Patent No. 6310193
                                                                                                                  ||| || :|||:|| | | OKLLKAYFEKLGVKNDF 442
                                                                                          OKLONAYLDKLGMKNAF 437
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

CMPITER: IBM Compatible
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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Gaps

Mismatches 126; Indels

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200; Conservative
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                                                                                                                        121 SANAKYFVFESDEYERHFMPYHDEYSIIINIDFDHPDYFTSLEDVFNAFNDYAKQITKGL 180
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                                                                                                                                                                          201 IAWGDDEHLRKIEADVPIYYYGFK-DSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQ 259
                                                                                                                                                                                                                                                                  320 ISATIETARKKYPHKEVVAVFOPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRE-NT 378
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                                                         61 DQNGISYKRYHEFLGSFWRDFVSMGVAGAHGKTSTTGMLSHVLSHITDTSFLIGDGTGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 116, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
   HQMGHKVQGSDVEKYYFTQRGLEQAGITILPFDEKNLDGDMEIIAGNAFRPDNNVEIAYA
                                   81 HQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVMNGDKKTSFLIGDGTGMG
                                                                                                      141 LPESDYFAFEACEYRRHFLSYKPDYAIMINIDFDHPDYFKDINDVFDAFQEMAHNVKKGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM, MSDOS Version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: SEQ ID NO: 116:
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TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 422 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-8512
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COMPUTER READABLE FORM:
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ULE TYPE: protein
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Best Local Similarity
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US-09-536-784-116
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SEQUENCE
US-09-536-784-116
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                       140
                                                                                                                                                                  61 DONGISYRRYHRFLGSFWRDFVSMGVAGAHGKTSTTGMLSHVLSHITDTSFLIGDGTGRG 120
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                                                                22 HDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMVVIQGNAF-ASSHEEIVRA
                                                                                                                                81 HQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVMNGDKKTSFLIGDGTGMG
                                                                                                                                                                                                                             141 LPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDINDVFDAFQEMAHNVKKGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 FGRHNIMMATAVIGLLYTAGFDLNLVREHLKTFRGVKRRFTEKIVNDTVIIDDPAHHPTE
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUMBUTER: DC, NOR, 130,000, COMBUTER: PC
OPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
FILING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
FILING DATE: 10,000, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6914, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 291 amino acids
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STATE: Massachusetts
COUNTRY: USA
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2712
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                                                                  345
                                                                                      333 GFSGVGRRFQVQGEFELGEGNVKLVDDYGHPPKEVEATIKAARQSHPDRRLVWLFQPHRY 392
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                                                                                                                                                                         64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM 123
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                                                                  291 IFGGVKRRFN-----ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFOPHTF
                                                                                                                                                     346 SRIQAFLNEFAESLSKADRVFLCEIFGS-----IRENIGALTIQ------DLIDKIE
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32.1%; Pred. No. 2.2e-43;
ive 78; Mismatches 185;
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US-09-540-236-2712
Sequence 2712, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
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Best Local Similarity 32.1%;
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2712
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US-09-489-039A-12280
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US-09-328-352-5023
Sequence 5023, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION UNMERR: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGTAF 243
                                                                                                                                                                                                                                                                                                                                                                             VIQCNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM 123
                                                                                                                                                                                                                                                                                                                   13 YHFVGIKGSGMSSLALVIJHEQGLNVQGSDIEKYFTQRDLEKANITILPFNADNVKPGMT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 HIHFVGIGGAGMCGIAEVLANQGYKISGSDIKASKTTQ-QLEENGIKVYIGHEAENIKNA
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                                                                                                                                                                                                                                                                                      4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
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                                                                                                                                                                                                    Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86; Mismatches 171; Indels
                                                                                                                                                                                                                                                58; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.5%; Score 967; DB 4; llarity 63.8%; Pred. No. 2.7e-86; Conservative 43; Mismatches 58
                                                                                           NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...291
SEQUENCE DESCRIPTION: SEQ ID NO: 6914:
                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 34.13
Matches 154; Conservative
        HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                          Local Similarity
les 178; Conserv
                                                                                                                                                            US-09-107-532A-6914
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US-09-328-352-5023
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                                                                           FEATURE
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Matches
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                             64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM 123
                                                                                                                                                                                                                                                                                                                            124 -NGDKKTSFLIGD-----GTGMGLPESDYFAFBACEYRRHFLSYKPDYAIMTNIDFDH-P 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 TNIKBALETFGGVKRRFN----ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 EAIVQGLSGFQGVGRRFQVYGELQVEGGSVMLVDDYGHHPREVAAVIKAIRGGWPERRLV 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 AVFOPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLIN 397
                                                                                                                                                                                                     5 HFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFDANNIKEDMV 63
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                                                                                                                                                            26;
                                                                                                        21.5%; Score 490; DB 4; Length 513; 30.9%; Pred. No. 2.9e-39; Live 77; Mismatches 195; Indels
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20.9%; Score 475; DB 4; Length 488;
Best Local Similarity 28.0%; Pred. No. 8e-38;
Matches 132; Conservative 86; Mismatches 183; Indele
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PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6951
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; Sequence 6951, Application US/09543681A
; Patent No. 6605709
                 ; TYPE: PRT:
; ORCANISM: Pseudomonas aeruginosa
US-09-252-991A-24196
                                                                                                                              Best_Local Similarity 30.9%
Matches 147; Conservative
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                 Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12280
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT PAPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OS/0094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OS/0094,190
NUMBER: OS/0094,190
SEQ ID NO 24196
LENGTH: 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 KEALETFGGVKRRFN---ETTIA-----NQVIVDDYAHHPREISATIETARKKYPHKE 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 DFDHPD-YFKDINDVFDAFQEMAHNVK--KGIIAWGDDEHLRKIEADV--PIYYYGFKDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                                                            21.9%; Score 499; DB 4; Length 492;
30.0%; Pred. No. 3.6e-40;
Live 86; Mismatches 192; Indels
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Sequence 12280, Application US/09489039A
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 30.03
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                             US-09-489-039A-12280
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAFITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
                                                                                                                                                                                                  Sequence 4942, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
PAPLICANT: GATY I. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/08/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 475
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    345 LRRVIAIFQPHRFSRLBECLQTFPKAFQEADEVILTDVYSAGESPRESIILSDLAEQIRK 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSHVMN-GDKKTSFLIGDGTGMGLPES-----DYFAFEACEY-----RRHFLSYKPD 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 RISLEANEKAALSAELISIDGSHFKVLENGNVIGEVKWSMTGQHSVANALATIAAAQHVG
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                                                                                           18.3%; Score 4..., 3.6e-32; 29.2%; Pred. No. 3.6e-32; Indels rive 75; Mismatches 202; Indels
                                                                   393 ASLI-----NEDSINVLEOF--DNAVILFMGAGDIOKLONAYLD
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Patent No. 6673910
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.2%
Matches 135; Conservative
                                                                                                                                                                   RESULT 12
US-09-328-352-4942
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US-09-328-352-4942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 978, Application US/09198452A
BATENT NO. 65529294
GENERAL INFORMATION:
APPLICANT: Griffale, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: On treatment of infection
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT APPLICATION NUMBER: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                    ---MNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNID 172
                                                                                    223
                                                                                                                                                                 ---FDVYVDGEFYDHFLSPQYGDHTVLNALAV 271
                                                                                                                                                                                                SEDADVRITHYE---OKGAQGFFTISREDMPDIDVVINAP------GRHNALNATAA 301
                                                                                                                                                                                                                                           IAISYLEKLDVINIKEALETFGGVKRRFN------ETTIANQVIVDDYAHHPREIS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 MVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 V-MNGDKKTSFLIGDGTGMGLP-----ESDYFAFEACEYRRHFLSYKPDYAIMTNI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GY--SPECQIHIVSYNOKAW-----QSHFSFTFLGQEYQDIELNIPGQHNAANAAACG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HKEVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                    142 YAQAGLDPTFVNG----GLVKSAĞTHARLGCSRYLIAEADESDASFLHLQPMVAVVTNIE
                                                                                                     FDHPD-YFKDINDVFDAFQEMAHNVKKGIIAWG-----DDEHLRKIEADVPIXY--YGF
                                                                                                                                                                                                                                                                                                                           ATIETARKKYPHKEVVAVFOPHTFSRTQAFLNEFAESLSKADRVFLCEIFGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 YHFIGIGGIGMSALAHILLDRGYEVSGSDLYESY--TIESLKAKGARCFSGHDSSHVPHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQY-----GDHTVLNALAVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDI-ENYVFTEVALRNKGIKILP-FDANNIKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :| :| ::::: | : | DNEHLNNYAGNLDNLVQVIQDFSRKV-----TDLNKVFINGDCPILKGNVQGISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISYLEKLOVINIKEALETFGGVKRRFNETTIANQ-VIVDDYAHHPREISATIETARKKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFDH-PDYFKDINDVFDAFQEMAHNVKKGIIAWGDDEHLRKI--EADVPI----YYY
                                                                                                                                                                                                                                                                                                                                                                                                                                       422 DSRSLCRTIRQRGKLDPIWVSDVENISSILAGVLTDNDLVLVQGAGNIGKI 472
                                                                                                                                                                                                                                                                                                                                                                                                       374 -IRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDIQKL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.7%; Score 470; DB 4; Length 81 28.2%; Pred. No. 5.5e-37; tive 89; Mismatches 181; Indels
                                                                                                                                                              KDSDDIYAQNIQITDKGTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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Sequence Notes, Application US/09489039A

Factor No. 6610836

GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA.
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR SEQ ID NOS: 14342
SEQ ID NO 8987
                                                                                    60 EDMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFL-GQIIDQYTSVAVTGAHGKTSTTGL 118
                                                                                                                                                                                   LSHVMNG-DKKTSFLIGDGTG-----MGLPESDYFAPEACEY-----RRHFLSYKPDY 165
                                                                                                                                                                                                                                                                                                     LRKIEADVPIYYYGFKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNA 268
                                                                                                                                                                                                                                                                                                                        -----YTG--ETGDWQAK--KISNDSSHFAVFHKGEQVGEVCWGLSGEHNMQNG 296
                                                                                                                                                                                                                                                                                                                                                                        269 L-AVIAISYLEKUDVINIKEALETFGGVKRRFNETTIANQV-IVDDYAHHPREISATIET 326
                                                                                                                                                                                                                                                                                                                                                                                                   166
              HYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILP-FDANNIK-- 59
                                     14 HIHILGICGTFWGSLAILARAKGHKVTGSDANVYPPMSTLLENQGIELIEGYDPQQLEPA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 IMTNIDFDHPDYFKDINDVFDAFQEMAHNV--KKGIIAWGDDEHLRKIEADVPIYYYGFK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 ILNNLEFDHADIFDDLKAIQKQFHHLVRIVPGKGKILLPENDINLKQVMA------MGCW 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 SEQELVGEQGHWQAKKLINADASQWEVILLDGEKVGEVKWALVGEHINGHMGINGIAAARHVG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                166 AIMTNIDFDHPDYFXDINDVFDAFQEMAH-------NVKK--GIIAWGDDEH
                                                                                                                                                                                                                                                     62 MVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQII--DQYTSVAVTGAHGKTSTTGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 DSDDI----YAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 SHVMNG-DKKTSFLIGDGTG-----MGLPESDYFAFRACEY------RRHFLSYKPDYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 HFVGIKGSGMSSLAQIMHDLGHRVQGSDIENYVFTEVALRNKGIKILP-FDANNI--KED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 ARKKY-PHKEVVAVFQPHTFSRTQAF-LNEFAESLSKADRVFL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.8%; Score 358.5; DB 4; 27.2%; Pred. No. 1.8e-26; tive 78; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 27.2%
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-09-489-039A-8987
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Batent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-011

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5705
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                                                                                                                                                                                                                                                                                          60 EDMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQII--DQYTSVAVTGAHGKTSTTG 117
                                                                                                                                                                                                                                                                                                                      ----YPAFEACEY---- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                      --RRHFLSYKPDYALMTNIDFDHPDYFKDINDVFDAFQEMAHNV-KKGIIAWGDDEHLRK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEADVPIYYYGFKDSDDIYAQNIQIT-DKG---TAFDVYVDGE------FYD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 IPANTP-----SLETTLDKGVWTTVVRTSLNGDAEWQAKLDANDGSSFWV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 HFLS-----PQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETTIAN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVIV-DDYAHHPREISATIETARKKYPHKEVVAVPQPHTFS-RTQAFLNEFAEGLSKADR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 VFLCEIFG---SIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDIQ 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 VIWYEPQGLIWGLKEAIGSTPNQRVLDSIN--AII--EHIKTYAKAGDAII-MSNGDFE 460
                                                                                                                                                                                                                     3 HYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILP-FDANNI--K 59
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                           95;
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                                                                                                                                                     DB 4; Length 473;
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                                                                                                                                              Query Match
17.0%; Score 386.5; DB 4; Length
Best Local Similarity 27.8%; Pred. No. 3.5e-29;
Matches 136; Conservative 82; Mismatches 177; Indel8
                                                                                                                                                                                                                                                                                                                                                                   LLSHVMN-GDKKTSFLIGDGTGMGLPESD-
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2891
LENGTH: 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 KLQNAYLDKL 431
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                                                                                         ; ORGANISM: M.catarrhalis
US-09-540-236-2891
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338 AVFOPHTFSRTOAFL-NEFAESLSKADRVFLCE-
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382	416		
330 AVECENTIONIONE DEFENDAMENTE TO 1 382	357 AVLEPRSNIMKMGVCKDDLAPSLGRADEVFLLQPQHIPWQVAEVARACVQPAHWSADVDT 416	383 IQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDIQKLQNAYLDKLGMKNA 436	417 IAEMVVKTAHPGDHILVMSNGGFGGIHQKLLDKLAQKAA 455
0	35	38	41

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Search completed: June 3, 2004, 14:41:12 Job time: 23 secs

Sequence 71315, A
Sequence 51682, A
Sequence 53624, A
Sequence 51682, A
Sequence 61427, A
Sequence 61427, A
Sequence 6121, A
Sequence 6121, A
Sequence 63073, A
Sequence 5173, A
Sequence 6518, A
Sequence 6618, A

Sequence 14079, A

Sequence:

Searched:

Database

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FILE REPERENCE: PBS60

FILE REPERENCE: PBS60

FILE REPERENCE: PBS60

CURRENT APPLICATION NUMBER: US/09/925,637

CURRENT PILING DATE: 2001-08-10

FRIOR FILING DATE: 2001-08-10

FRIOR FILING DATE: 2001-08-31

FRIOR FILING DATE: 1999-09-01

FRIOR PRICING DATE: 1999-09-01

FRIOR APPLICATION NUMBER: US 66/151,933

FRIOR FILING DATE: 1997-01-03

FRIOR FILING DATE: 1997-01-03

FRIOR FILING DATE: 1997-01-03

FRIOR FILING DATE: 1997-10-20

FRIOR FILING DATE: 1997-10-20

FRIOR FILING DATE: 1996-01-06

FRIOR FILING DATE: 1996-01-06

FRIOR FILING DATE: 1996-01-06

SEQ ID NO 2

SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 2275; DB 9; Length 437; 100.0%; Pred. No. 2.9e-198; ive 0; Mismatches 0; Indels 0
2. US-10-282-122A-74073
2. US-10-282-122A-71315
2. US-10-282-122A-51215
2. US-10-282-122A-51682
2. US-10-282-122A-51682
2. US-10-282-122A-44665
2. US-10-282-122A-44665
2. US-10-282-122A-61427
2. US-10-282-122A-65124
2. US-10-282-122A-65137
2. US-10-282-122A-55082
2. US-10-282-122A-55082
2. US-10-282-122A-55082
2. US-10-282-122A-55082
2. US-10-282-122A-56082
2. US-10-282-122A-66650
2. US-10-282-122A-66650
2. US-10-282-122A-66650
2. US-10-282-122A-66550
2. US-10-282-122A-68521
2. US-10-282-122A-68521
2. US-10-282-122A-68521
2. US-10-282-122A-68521
2. US-10-282-122A-68521
2. US-10-282-122A-68521
2. US-10-282-122A-76478
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Patent NO. US20020103338A1
GENERAL INFORMATION:
APPLICANT: Choi
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Best Local Similarity 100.
Matches 437; Conservative
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US-09-925-637-2
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Sequence 2, Appli
Sequence 43780, A
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                                                                                                                          3, 2004, 14:40:41; Search time 48 Seconds (without alignments) 2561.354 Million cell updates/sec
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                                                                                                                                                                                                                                    1 MTHYHFVGIKGSGMSSLAQI......GDIQKLQNAYLDKLGMKNAF
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-10-084-205-2

6 US-10-712-713-2

2 US-10-282-122A-43780

US-09-815-242-12293

US-10-282-122A-71178

2 US-10-282-122A-46331

US-10-282-122A-46331

US-09-815-242-10870

US-09-815-242-10870

US-09-815-242-10870

US-10-282-122A-57651

US-10-282-122A-57651

US-10-282-122A-7651

US-10-282-122A-77551

US-10-282-122A-77551

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US-09-815-22A-77551
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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99.6
99.6
87.3
64.6
63.2
63.2
61.4
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Perfect score:
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Result

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301 ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS 360
                                                                                                                                                                                                                                                                Sequence 2. Application US/10712713
; Publication No. US20040082002A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil
; TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; TILE REFERENCE: PES151
; CURRENT APPLICATION NUMBER: US/10/712,713
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR PELING DATE: 2000-08-31
; PRIOR PILING DATE: 2000-08-31
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 2
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                                                                         361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI
                                                                                               361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI
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                                                                                                                                                 OKLONAYLDKLGMKNAF 437
                                                                                                                                                                                    421 OKLÓNAYLDKIGMKNAF 437
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 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120
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Publication No. US20330049648A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT PELICANTON NUMBER: US/10/084,205
CURRENT FILING DATE: 2002-02-28
PRIOR PELICATION NUMBER: PCT/US00/23773
PRIOR APPLICATION NUMBER: 60/151,933
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PATENTH UP: 3.1
SEQ ID NO 2
LENGTH: 437
                                                                                                                                  TAFDVYVDGEFYDHFLSPQYGDTTVINALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
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100.0%; Score 2275; DB 14; Length 437;
Best Local Similarity 100.0%; Pred. No. 2.9e-198;
Matches 437; Conservative 0; Mismatches 0; Indels 0;
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241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 300
                                                                                                                                                                                                         420
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                                                                                                      301 ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS
                                                                                                                                                                                                     361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI
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APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Boward

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Deckaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-11-27

PRIOR PRING DATE: 2000-11-27

PRIOR PLILING DATE: 2000-11-27
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99.5%; Pred. No. 1.6e-197;
tive. 1; Mismatches 1;
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Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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Best Local Similarity 99.53
Matches 435; Conservative
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PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-010-23

PRIOR PRILING DATE: 2000-010-23

PRIOR PRILING DATE: 2000-110-23

PRIOR PRILING DATE: 2000-110-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR PRIOR FILING NOS: 78614

SOFTWARE: PALENTIN VESTON 3.1

SEQ ID NOS: 78614

SEQ ID NO 43780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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                                                                                    Sequence 43780, Application US/10282122A
Publication No. US20040029129A1
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Apone, Cheryl
APPLICANT: Apelbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Cyskind, Judith
APPLICANT: Tawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
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APPLICANT:
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128 HVWNGDXKTSFLIGDGTGMGLPESDYFAFBACEYRRHFLSYKPDYAIMTNIDFDHFDYFK 187
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                                                                                                      248 TAFDVYVDGBFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-23
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2010-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2001-02-09
                                                                                                                                                                                           241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
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                                                                181 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 71178, Application US/10282122A Publication No. US20040029129A1
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; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-71178
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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SEQ ID NO 71178
LENGTH: 437
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Forsyth, R.
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DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 240
                                                                                                      241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIALSYLEKLDVINIKEALETFGGVKRRFN 300
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APPLICANT: Oblsen, Kari L.
APPLICANT: Trawich, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawich, John D.
APPLICANT: Trawich, John D.
APPLICANT: Trawich, John D.
APPLICANT: Tramanco, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: PECKARYOCES
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/203
PRIOR APPLICATION NUMBER: 60/203
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PRICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
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Pred. No. 1.6e-197;
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Patent No. USZ0020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12293
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Best Local Similarity 99.5%;
Matches 435; Conservative
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US-09-815-242-12293
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LENGTH: 444
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FILING DATE: 2000-12-22
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT TIING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR FILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-19-09
FRIOR FILING DATE: 2000-19-09
FRIOR FILING DATE: 2000-19-09
FRIOR FILING DATE: 2000-19-09
FRIOR APPLICATION NUMBER: 60/242,578
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
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      Length 437;
                                      Indels
     87.3%; Score 1985; DB 12;
84.7%; Pred. No. 7.3e-172;
iive 43; Mismatches 24;
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Publication No. US20040029129A1
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olleen, Kari
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
Xu, H.
                                      Conservative
Query Match
Best Local Similarity
Matches 370; Conserv
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION UNMERS: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                           Gape
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46331
LENGTH: 436
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                                                                                                                                                                                                                                                                                                                         64.6%; Score 1470; DB 12;
64.7%; Pred. No. 5.4e-125;
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                ORGANISM: Bacillus anthracis
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Matches 279; Conservative
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Wall, Daniel Trawick, John D. Carr, Grant J. Yamamoto, Robert T.

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69 VIAGNAFPDTHEEIARAIELGAEVIRYHDFIARFIEPYTSIAVTGSHGKTSTTGLLAHVL 128
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
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60.9%; Pred. No. 4.1e-122;
ative 79; Mismatches 86;
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Best Local Simi:
Matches 259; (
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80 VIAGNAFPDTHEBIARAIELGAEVIRYHDFIARFIEPYTSIAVTGSHGKTSTTGLLAHVL 139
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

FILTE OF INVENTION: Prokaryotes

FILTE OF INVENTION: PROKARYOTES

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT APPLICATION NUMBER: 00/10-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR PRIOR FILING DATE: 2000-10-23

PRIOR PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PRIOR DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/253,931

PRIOR APPLICATION NUMBER: 60/253,931

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16
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Best Local Similarity 60.7%; Pred. No. 1.2e-121;
Matches 258; Conservative 79; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10870 LENGTH: 456
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US-09-815-242-10870
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RESULT 11 US-10-282-122A-57651 is Sequence 57651, Application US/10282122A is Publication No. US20040029129A1

Sequence 10870, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.

US-09-815-242-10870

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APPLICANT: Foreyth, R.
APPLICANT: Anamanoco, Koobert
APPLICANT: Xu, H.
TITLE OF INVENTION Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR PILING DATE: 2000-03-21
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR PILING DATE: 2000-05-26
FRIOR PILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: 60/230,335
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-09-09
FRIOR PILING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/245,578
FRIOR FILING DATE: 2000-10-23
FRIOR PILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2000-12-22
FRIOR PILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2000-12-22
FRIOR PILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2001-12-29
FRIOR PILING DATE: 2001-12-29
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FRIOR FILING DATE: 2001-12-29
FRIOR PILING DATE: 2001-12-16
FRIOR PILING DATE: 2001-12-16
         364 RVFLCEIFGSIRENTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDIQK 422
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NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                        Sequence 60988, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
Wall, Daniel
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Best Local Simi:
Matches 255;
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APPLICANT:
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PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PRILING DATE: 2000-05-62

PRIOR PILING DATE: 2000-05-66

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-01-02

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-3

PRIOR PILING DATE: 2000-12-3

PRIOR PILING DATE: 2000-12-3

PRIOR PILING DATE: 2001-12-7

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-16

NUMBER OF SEO IN NGC: 786-14
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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US-10-282-122A-57651
Wang, Liangsu

Zamudio, Carlos

Malone, Cheryl

Haselbeck, Robert

Ohlsen, Kari

Zyskind, Judith

Wall, Daniel

Trawick, John

Carr, Grant
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SOFTWARE: Patentin version 3.1
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Forsyth, R.
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Best Local Similarity 60.6*
Matches 260; Conservative
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LENGTH: 444
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APPLICANT:
                           Query Match
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APPLICANT: Forsyth, R.
APPLICANT: Yu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-02-06
PRIOR PLING DATE: 2001-02-06
241 TKFDVYHREEFLSSFEIPAYGDHNVLNALSVIALCDYEGLPVEDVKNELKTFEGVKRRFS 300
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                                                                            181 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 240
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SOFTWARE: PatentIn version 3.1
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Publication No. US20040029129A1
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; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74395
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APPLICANT: Wang, Liangsu
APPLICANT: Tamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Othern, Kari
APPLICANT: Othern, Kari
APPLICANT: Wall, Daniel
APPLICANT: Travick, John
APPLICANT: Travick, John
APPLICANT: Travick, John
APPLICANT: Tamancto, Robert
APPLICANT: Foreyth, R.
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                                                     Gaps
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  Length
                                                     Indels
50.1%; Score 1139; DB 12;
50.7%; Pred. No. 7.4e-95;
tive 82; Mismatches 128;
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PELING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-11-23
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                     Matches 218; Conservative
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                            Similarity
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completed: June 3, 2004, 14:46:36
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; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13507
           FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                               Length 443;
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper of Software: Patentin version 3.1
SEQ ID NO 72179
LENGTH: 443
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| Patent No. US20020061569A1
| GENERAL INFORMATION:
| APPLICANT: Haselbock, Robert
| APPLICANT: Ohlsen, Kari L.
| APPLICANT: Wall, Daniel
| APPLICANT: Trawick, John D.
| APPLICANT: Trawick, John D.
| APPLICANT: Trammoto, Robert T.
| APPLICANT: Trammoto, Robert T.
| APPLICANT: Yamamoto, Robert T.
| APPLICANT: Yamamoto, Robert T.
| APPLICANT: Xu, H. Howard
| TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                           Query Match 49.8%; Score 1132.5; DB 12; Lengt
Best Local Similarity 50.7%; Pred. No. 2.9e-94;
Matches 218; Conservative 84; Mismatches 125; Indels
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                ORGANISM: Streptococcus mutans
US-10-282-122A-72179
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426 LYERSFEELL 435
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64 VIQGNAF-ASSHERIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 49.8%; Pred. No. 4.9e-93;
Matches 213; Conservative 84; Mismatches 127;
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SCATANARE: FastSEQ for Windows Version 4.0
LENGTH: 444
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	Copyright	

- protein search, using sw model OM protein

June Run on:

3, 2004, 14:38:01 ; Search time 20 Seconds (without alignments) 2101.785 Million cell updates/sec

US-10-712-713-2 2275 Title: Perfect score:

1 MTHYHFVGIKGSGMSSLAQI.....GDIQKLQNAYLDKLGMKNAP Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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	Description	UDP-N-Aacerylmuram	UDP-N-acetylmurama	UDP-N-acetylmurama	UDP-N-acetyl muram	UDP-N-acetyl muram	hypothetical prote	Ε	UDP-N-acetylmurama	UDP-N-acetylmurama	UDP-n-acetylmurama	hypothetical prote	UDP-N-acetylmurama	UDP-N-acetylmuramo	UDP-N-acetylmurama	UDP-N-acety1murama	UDP-N-acetylmurama	UDP-N-acetyl-muram	UDP-N-acetyl-muram	UDP-N-acetylmurama	UDP-N-acetylmurama	probable UDP-N-ace	muramate-Ala ligas	UDP-N-acetylmurama						
SUMMAKIES	ID	H89958	C69662	H84055	AE1638	AE1275	H86879	D98043	B95177	F97296	C71679	C97741	A81777	H70201	B81201	A87565	B70418	AF2833	B97611	A12438	B81737	AF3324	CEECAM	G90640	G85491	AF0518	D83094	C71338	G86603	D72022
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d	Query Match	100.0	63.2	60.1	59.6	59.0	51.9	49.2	49.1	28.2	24.9	24.9	24.1	23.6	23.5	23.5	22.9	22.5	22.5	22.0	21.8	21.6	21.6	21.6	21.6	21.6	21.5	21.4	20.7	20.7
	Score	2274	1438	1368	1355	1342	1180	1119	1117	641.5	266	565.5	548	538	535	534	521	513	513	500.5	496	492.5	491	491	491	490.5	490	487	470	470
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UDP-N-acetylmurama	UDP-N-acetylmurama	probable muramate-	probable UDP-N-ace	UDP-N-acetylmurama	UDP-N-acetylmurama	UDP-N-acetylmurama	UDP-N-acetylmurama	UDP-N-acetylmurama	UDP-N-acetylmuramo	probable murC prot	UDP-N-acetyl-muram	udp-n-acetylmurama	UDP-N-acetylmurama	UDP-N-acetylmurama	UDP-N-acetylmurama
A10068	A72402	A71475	T35852	E64185	D82081	E82763	C81308	C84955	876722	D70579	E87023	B71917	G64597	B64002	F81904
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491	457	803	462	475	206	477	432	484	202	494	495	449	449	453	458
20.4	20.4	20.4	20.3	20.2	20.2	20.0	19.9	19.6	19.5	18.5	18.4	18.0	17.7	17.3	17.1
465	463	463	461.5	460.5	460.5	455	453.5	446	442.5	420	417.5	410	403	392.5	390
30	31	32	33	34	35	36	37	38	39	0	11	2	13	4	2

ALIGNMENTS

	Staphyloc		#toxt cb)
	[imported] -		n 10-May 2001	
	-alanine ligase	ccus aureus	sequence revisio	\
19958)P-N-Aacerylmuramate-alanine ligase [imported] - Staphyloc	Species: Staphylococcus aureus	Date: 10-May-2001 #Bequence revision 10-May-2001 #text of	Propert . no. pagera

RESULT 1
H89958
UDP-N-Aacerylmuramate-alanine ligase [importe.,
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision_10-May-2001 #text_change 22-Oct-200-2001 #text_cha

A, Accession: H89958 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-437 < KUR>

A,Cross-references: GB:BA000018; PID:g13701535; PIDN:BAB42829.1; GSPDB:GN00149
A,Experimental source: strain N315
C;Genetics:
A;Gene: murc
C;Superfamily: UDP-N-acetylmuramate-alanine ligase

Gaps Length 437; Indels Query Match 100.0%; Score 2274; DB 2; Best Local Similarity 99.8%; Pred. No. 1.4e-148; Matches 436; Conservative 1; Mismatches 0;

1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE

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120 120 180 240 HVMNGDKKTSFLIGDGTGMGLPESDYFAPEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 180 9 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE 61 DMVVIQGNAFASSHERIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 121 121 61 ద Š 엄 ò 원

181 DINDVEDAPQEMAHNVKKGIIANGDDEHLRKIEADVPIYYYGFKOSDDIYAQNIQITDKG 240 241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRFFN 300 TAPDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 300 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 181 241 301 301 g g Š 셤 ਠੋ ઠ

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UDP-N-acetylmuramate-alanine ligase murC [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-433 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06967.1; GSPDB:GNO(
A;Experimental source: strain C-125
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nutcleic Acids Rss. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: H84055
A;Actus: preliminary
A;Molecule rype: DNA
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| HVLGSHCPTSFLIGDGTGKGAADSHYFVFEACEYRRHFLNYRDDYCIMTNIDFDHPDYFD 180
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241 TTFDVFVRNTFYDTFYIPAYGHHNVLNSLAVIALCHYEEIDSSIIKHALKSFGGVKRRFN 300
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                                                                                                              61 DMVVIQGNAFASSHEBIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS
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                                                                          ETTIANOVIVDDYAHHPREISATIETARKKYPHKEVVAVFOPHTFSRTQAFLNEFAESLS
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59.3%; Pred. No. 2.2e-86;
tive 69; Mismatches 105;
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C;Superfamily: UDP-N-acetylmuramate-alanine ligase
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Matches 253; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      C; Species: Bacillus subtilis
C; Date: 05-Dec-1997 #text_change 03-Jun-2002
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Jun-2002
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Jun-2002
C; R; C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Jun-2002
C; Bron, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A; Britch, S.; Bruschi, C.Y.; Entian, K.D.; Errington, J.; Fubret, C.; Ferrari, B.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Roche, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Setgunhi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Yasumoto, K.; Yata, K.; Yoshida, M.
A; Authors: Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshida, M.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Riffleer of Danchin, A.; Reference number: A69580; MUD:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary, nucleic acid sequence not shown; translation not shown A;Nolecule type: DNA A;Nolecule type: GNA A;Nolecule type: Statin 168 A;Nolecule type: Snalecule type: Snalecu
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C,Superfamily: UDP-N-acetylmuramate-alanine ligase
C,Keywords: ATP binding; cell division; cell wall; ligase; peptidoglycan biosynthesis
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   361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVVLFMGAGDI 420
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A;Residues: 85-432 - CVAR>
A;Cross-references: EMB1:L31845; NID:g556013; PIDN:AAB40043.1; PID:g556014
A;Experimental source: strain 168, substrain Marburg
                                                                                                                                                                                                                                                                                                       C69662
UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8) murC - Bacillus subtilis
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A;Accession: AE1275
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesiduss: 1-47 < CLA>
A;Cass-references: GB:NC_003210; PIDN:CAC99683.1; PID:gl6411034; GSPDB:GN00177
A;Experimental source: strain EGD-e
A;Genetics:
A;Genetics:
A;Genetics: MurC
C;Superfamily: UDP-N-acetylmuramate-alanine ligase
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.0%; Score 1342; DB 2; Length 4 Best Local Similarity 59.7%; Pred. No. 1.4e-84; Matches 255; Conservative 64; Mismatches 108; Indels
A; Reference number: AB1077; MUID:21537279; PMID:11679669
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C;Superfamily: UDP-N-acetylmuramate-alanine ligase
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Daccession: AE1275
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
                                                                                  Cipecies: Listeria innocua
Cipecies: Listeria innocua
Cipecies: Listeria innocua
Cipecies: Z7-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
Cipate: Z7-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
Cipate: Z7-Nov-2001
Cipate: Z8-Nov-2001
Cipate: Z8-
                                                  UDP-N-acetyl muramate-alanine ligases homolog murc [imported] - Listeria innocua (strain
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UDP-N-acetyl muramate-alanine ligases homolog murC [imported] - Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Residues: 1-447 <GLA>
A.Gross-references: GB:AL592022; PIDN:CAC96877.1; PID:g16414133; GSPDB:GN00178
A.Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLTIAGNAPPDTHEEIERANELMLPVIRYHKFLGOLIDGYTSIAITGSHGKTSTTGLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HVMNGDKXISFLIGDGIGMGLPESDYFAFBACEYRRHFLSYKPDYAIMINIDFDHPDYFK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.6%; Score 1355; DB 2; Length 447; 60.2%; Pred. No. 1.8e-85; tive 63; Mismatches 107; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: UDP-N-acetylmuramate-alanine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.2%
Matches 257; Conservative
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hypothetical protein murc (imported) - Lactococcus lactis subsp. lactis (strain IL1403) hypothetical protein murc (imported) - Lactococcus lactis subsp. lac
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us-10-712-713-2.rpr

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G;Species: Streptococcus pneumoniae
G;Date: 03-Aug-2001
#sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: B95177

G;Accession: B95177

G;Accession: G;Barbence_revision 03-Aug-2001 #text_change 24-Aug-2001

G;Date: 03-Aug-2001

#sequence_revision 03-Aug-2001

#inckey, Minte, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
G;Gience 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005672; PIDN:AAK75611.1; PID:g14973011; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                           UDP-N-acetylmuramate-alanine ligase [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 ADRVFLCEIFGSIRE-NTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGD 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 NDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFK-DSDDIYAQNIQITDKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 YHFIGIKGSGWSALALMLHQWGHKVQGSDVEKYYFTQRGLEQAGITILFFDEKNLDGDME
                                                         245 TFTVHFRGQNLGQFHIPTFGRHNIMMATAVIGLLYTAGFDLNLVREHLKTFAGVKRRFTE
                                                                                                                305 KIVNDTVIIDDFAHHPTEIIATLDAARQKYPSKBIVAVFQPHTFTRTIALLDDFAHALNQ
                                                                                                                                                                                                                 123 MNGDKKTSFLIGDGTGMGLPESDYFAFBACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDI
185 EDVFNAFNDYAKQITKGLFVYGEDAELRKITSDAPIYYYGFEAEGNDFVASDLLRSTTGS
                                    242 APDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEXLDVTNIKEALETFGGVKRRFNE
                                                                                                                                                                                            362 ADRVFLCEIFGSIRE-NTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SP1521
C;Superfamily: UDP-N-acetylmuramate-alanine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 49.8*
Matches 213; Conservative
                                                                                                                                                                                                                                                                              420 IQKLQNAY 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-444 <KUR>
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; J.; Bu., D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; J.; Sun, P.M.; Winkler, M.S.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A;Reference number: A97872; MuID:21429245; PMID:11544234
A;Accession: D98043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8) [imported] - Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Cross-references: GB: AE007317; PIDN: AAL00177.1; PID: 915459022; GSPDB: GN00174
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                                                                                                                                                                                                                                             303 TIANOVIVDDYAHHPREISATIETARKKYPHKEVVAVFOPHTFSRTOAFINEFAESISKA 362
                                                                                                                                                                                                                                                                                                                                                                                                         319 KVGETVIIDDPAHHPTEIEATLDAARQKYPDREIVAVFQPHTFTRTIAFADEFAEVLDHA 378
                                                                                                    138
                                                                                                                                           MNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDI 182
                                                                                                                                                                                                                         NDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGTA 242
                                                                                                                                                                                                                                                                                                     FDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNET 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Streptococcus pneumoniae
C.Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
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                                                                                    DRVFLCEIFGSIRE-NTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDI
                                                                 VIQGNAFASSHE-EIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHV
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49.2%; Score 1119; DB 2; Length 444;
Best Local Similarity 49.8%; Pred. No. 2.8e-69;
Matches 213; Conservative 84; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: UDP-N-acetylmuramate-alanine ligase C;Keywords: ligase
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| OKYELAF-EKL 448
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A.Molecule type: DNA
A.Residues: 1-444 <KUR>
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A; Reference number: A71630; MUID: 99039499; PMID: 9823893
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                                                                                                                                                                                          C; Species: Clostridium acetobutylicum
C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C; Accession: F97296
R; Nolling, U; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gibson, R.; Lee,
S; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A; Reference number: A96900; MUID:21359325; PMID:21359325
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                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE001437; PIDN:AAK81161.1; PID:g15026298; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum AFCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175
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UDP-n-acetylmuramate-alanine ligase (murC) RP247 - Rickettsia prowazekii
UDP-n-acetylmuramate-alanine ligase (murC) RP247 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Bate: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: C71679
                                                                                                                                                                     UDP-N-acetylmuramate-alanine ligase [imported] - Clostridium acetobutylicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -MNGDKKTSFLIG-----DGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 ALTEDVDPTILVGGNLDIINGNVLA-GKSDYFITEACEYKASFLEFYPYIGVILNIDADH
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                               420 IOKLONAY 427
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A;Molecule type: DNA
A;Residues: 1-458 <KUR>
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A;Accession: C71679
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Nolecule type: DAND>
A;Residues: 1-495 <AND>
A;Reperimental source: strain Madrid E
C;Genetics: murc; RP247
C;Superfamily: UDP-N-acetylmuramate-alanine ligase
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Cipacies: Rickettesia conorii
Cipate: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
Cipate: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
Cipate: 30-Sep-2001
Cipate: Addic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 23, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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A;Molecule type: DNA
A;Residues: 1-485 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL02869.1; PID:g15619392; GSPDB:GN00173
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 YYGEKDSDD--IYAQNIQITDKGTAFDVYVD-----GEFYDHFLSPQYGDHTVLNALAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 TYGI-DSEDAHIIAFNINTDIASSTFDVKISLPNVLGTTIIEKITIPTPGRHNILNSLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 -KYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 HFVGIKGSGMSSLAQIMHDLGHEVQGSD-IENYVFTEVALRNKGIKI-LPFDANNIKEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTT-----
                                                                                                                                                                                                                                                                                                                                                                                          5 HFVGIKGSGMSSLAQIMHDLGHEVQGSD-IENYVFTEVALRNKGIKILPFDA-NNIKEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                               17 HPIGIGGVGMSGIABILHNIGYKVQGSDLVENY--NTKRLESYGIKIFLGQAKQNIKNVS
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                                                                                                                                                                                                                                                                              Query Match 24.9%; Score 566; DB 2; Length 49
Best Local Similarity 33.3%; Pred. No. 3e-31;
Matches 158; Conservative 78; Mismatches 172; Indels
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C;Superfamily: UDP-N-acetylmuramate-alanine ligase
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R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998 A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

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A;Cross-references: GB:AE001180; GB:AE000783; NID:g2688755; PIDN:AAC67166.1; PID:g268876
A;Experimental source: strain B31
C;Superfamily: UDP-N-acetylmuramate-alanine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: H70201
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, P.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A; Muthors: Smith, H.O.; Venter, J.C.
A; Fitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; WUID:98065943; PMID:9403685
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                                                                                                                                                                                                                                                                               VINIKEALETFGGVKRRF---NETTIAN---QVIVDDYAHHPREISATIETARKKYPHKE 335
                                                                                                                                                                                            DHMDTYGHSVEKLHQAFIDFIHRMPFYGKAFLCI-DSEHVRAILPKVSKEYATYGLDDTA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: H70201
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UDP-N-acetylmuramate-alanine ligase (murC) homolog - Lyme disease spirochete C; Species: Borrelia burgdorferi (Lyme disease spirochete) C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIREN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 RKDISIFSYGSGDLSDPQISNIAVRSEYFCFS-----FLGLLNVELKTVLFHNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-ALAVIAIS-YLEK--LDVINIKEAL----ETFGGVKRRFNETTIANQVI-VDDYAHHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 SYKPDYAIMTNIDFDHPDYFKDINDVFDAFQEMAHNVKKG--IIAWGDDEHLRKIE----
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                                                                                 DIYAQNIQITDKGTAPDVYV-----DGEFYDHPLSPQYGDHTVLNALAVIAISYLEKLD
                                                                                                           VVAVPOPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKI-----
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                                                                                                                                                                                                                                                                                                                                                                459 LEPIYCENVADL.PEMLLINVLQ--DGDIVLNWGAGSINRVPAALLE 501
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Best Local Similarity 31.0%; Pred. No. 2.3e-29;
Matches 148; Conservative 91; Mismatches 155;
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A; Residues: 1-468 < KLE>
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R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.

A; Reference number: A81775; MUID: 20222556; PMID: 10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-506 <PAR>
A;Cross-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85279.1; PID:g738066
A;Experimental source: serogroup A, strain 22491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 SHVMN-GDKKTSFLIGD-----GTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKYPHKE----VVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQD 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIDKIEGASLINEDSINVLEQFDNAV-----ILFWGAGDIQKLQNAYLDKLGM 433
                                                                                                                                       ---GLLSHVMNG----DKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIM 168
                                                                                                                                                                        220 YYGFKDSDD--IYAQNIQITDKGTAFDVYVD-----GEFYDHFLSPQYGDHTVLNALAV 271
                                                                                                                                                                                                                                                                                                                                        IAISYLEKLDVINIKEALETFGGVKRRFNETTIA---NQVIVDDYAHHPREISATIETAR 328
                                                                                                                                                                                                                                                                                                                                                                                                                     HFIGIGGVGMSGIAEILYNLGYKVQGSDLVENY--NTKRLESYGIKIFLGHAEQNITNVS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MIHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILP-FDANNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNIDFDHPDYFKDINDVFDAFQEMAENVKKGIIAWG-----DDEHLRKIEADV---PIY
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                                                           VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTT-
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32.5%; Pred. No. 5.4e-30;
tive 79; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: UDP-N-acetylmuramate-alanine ligase
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135 FEAAGLCPTVINGGIINNKSTNAYLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 32.5
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: murc; NMA2061
C;Superfamily: UDP-N-
C;Keywords: ligase
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R 477
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                                                                                                                           UDP-NacetyImuramate-alanine ligase NMB0423 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B81201
K;Tettellin, H: Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, Qin, H; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:2017575; PMID:10710307
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GB:AE002398; GB:AE002098; NID:g7225640; PIDN:AAF40861.1; PID:g722564
A,Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Caulobacter crescentus
C;Dates: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: A87565
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VINIKEALETFGGVKRRF---NETTIAN---QVIVDDYAHHPREISATIETARKKYPHKE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHPD-YFKDINDVFDAFQEMAHNVK---KGIIAWGDDEHLRKI--EADVPIYYYGFKDSD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHMDTYGHSVEKLHQAFIDFIHRMPFYGKAFLCI-DSEHVRAILPKVSKPYATYGLDDTA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIYAQNIQITDKGTAFDVYV-----DGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLD 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIYATDIENVGAQMKFTVHVQMKGHEQGSFEVVINMP--GRHNVINALAAIGVALEVGAS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
419
                     1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILP-FDANNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 VTNIHFVGIGGVGMSGIAEVLHNLGFKVSGSDQARNAATE-HLGSLGIQVYPGHTAEHVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHVMN-GDKKTSFLIGD-----GTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDF
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--EDSINVLEQ--FDNAVILFMGAGD
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UDP-N-acetylmuramate-alanine ligase [imported] - Caulobacter crescentus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.5%; Score 535; DB 2; Length 46 Best Local Similarity 32.3%; Pred. No. 3.8e-29; Matches 150; Conservative 78; Mismatches 194; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: UDP-N-acetylmuramate-alanine ligase
378 TGALTIODLIDKIEGASLIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-469 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Residus: Preliminary
A;Mosique: 1.473 <STO-
A;Cross-references: GB:AB005673; NID:g13424109; PIDN:AAK24517.1; GSPDB:GN00148
C;Genetics: CC2546
C;Superfamily: UDP-N-acetylmuramate-alamine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 HTESRIQAFLNEFAESLSKADRVFLCEIFGSIRENIGALTIQDLIDKIE-----GASLI 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 DHPDYFKDINDVFDAFQEMAHNVK-KGIIA-WGDDEHLRKIEADVP---IYYYGFKDSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 IYAQNIQITDKGTAFDVYVD---GEF--YDHFLSPQYGDHTVLNALAVIAISYLEKLDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 NIKEALETFGGVKRRFNETTIANQV-IVDDYAHHPREISATIETARKKYPHKEVVAVFQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 HFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFDANNIKEDMV
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYISVAVTGAHGKTSTT
                                                                                                                                                                                                                                                                                                                    Length 473;
                                                                                                                                                                                                                                                                                                                                                           82; Mismatches 186; Indels
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.0%; Pred. No. 4.4e-29;
Matches 143; Conservative 82; Mismatches 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :: | :: | | :: | 431 NPTALPRLIAAEATSGDLVVLLGAGDI 457
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 3, 2004, 14:33:06; Search time 18 Seconds Run on:

{without alignments)
1264.148 Million cell updates/sec

Title: Perfect score:

US-10-712-713-2 2275 1 MTHYHFVGIKGSGMSSLAQI......GDIQKLQNAYLDKLGMKNAF 437

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched: 141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description			Btaphyloc	baciling	bacilius	_	oceanopac	bacillus	listeria			_		_					-	-				•					aquifex ae	σ	'n.	-	Q87wy6 pseudomonas
SUMMARIES		QI	MURC STAAM	MURC STAAU	MURC STAEP	MURC BACAA		MURC BACSU		MURC_BACHD	MURC_LISIN	MURC_LISMO	MURC_LACPL	MURC LACLA	MURC STRP3	MURC_STRPY	MURC STRP8	MURC STRR6	MURC_STRPN	MURC THETN	MURC CLOAB	MURC CLOPE	MURC FUSNN	MURC RICPR	MURC RICCN	MURC_NEIMA	MURC BORBU	MURC NEIMB	MURC CAUCR	MURC SHEON		MURC AGRIS	- 1	- 1	MURC_PSESM
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		Match Length	437	437	437	436	436	432	438	433	447	447	436	443	442	442	442	444	444	460	458	457	468	495	485	469	468	469	473	488	454	471	486	475	486
•	* Query	Match	100.0	99.1	87.3	64.6		63.2	60.7	60.1	59.6	59.0	56.5	51.9	50.1	50.1	49.9	49.2	49.1	30.8	28.2	27.5	26.2	24.9	24.9	24.1	23.6	23.5	23.5	22.9	22.9	22.5	٠	22.2	22.1
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Q8ym75 anabaena sp Q92nm0 rhizobium m Q7vmy1 haemophilus Q9p131 c murc/ddl Q8d227 wiggleswort Q8yi65 brucella me Q8d1v5 synechococc P59418 buchnera ap Q8x9y7 escherichia P17952 escherichia Q82998 salmonella	098kb4 rhizobium 1
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ALIGNMENTS

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Staphylococcus epidermidis.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
-!- SIMILARITY: Belongs to the murCDEF family.
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Matches 432;
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10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
                    PIR; H89958; H89958; H89958; HAWAP; MP 20046; -; 1.

InterPro; IPR000110; Mur_ligase.

InterPro; IPR005758; MurC.

InterPro; IPR00578; Mu
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Best Local Similarity 99.8%; Pred. No. 1.7e-142;
Matches 436; Conservative 1; Mismatches 0;
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                                                                                                                                                                                                                     HAWAP; MF_00046; -; 1.
InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR004578; Murr_ligase_C.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase; 1.
TIGRFAMS; TIGR01082; murc; 1.
Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
ATP-binding.
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437 AA, 49176 MW, E2FC7D79E6CF8361 CRC64;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8)
acetylmuramyl-L-alanine synthetase).
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-i- PATHWAY: Peptidoglycan biosynthesis.
-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- SUBCELLULAR: Belongs to the murCDEF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
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InterPro; IRRO00713; Mur_ligase.
InterPro; IRRO00713; Mur_ligase.
InterPro; IRRO00713; Mur_ligase.
InterPro; IRRO01001; Mur_ligase.
InterPro; IRRO0100578; Murc.
InterPro; IRRO100578; Murc.
IRRO INTO INTERPRO; INTE
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                                                                                                                                                                                                                                                                                                                                                                                              Bacillus anthracis (strain Ames).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=198094;
                                                                                                                                                                 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8)
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-!- FUNCTION: Cell wall formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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InterPro; IPR000713; Mur_ligase.

InterPro; IPR004013; Mur_ligase.

InterPro; IPR004019; Mur_ligase_C.

Ream; PF01225; Mur_ligase; 1.

Ream; PF02875; Mur_ligase; 1.

Refam; PF02875; Mur_ligase; 1.

Rigase; ATP-binding; Cell division; Cell wall;

Migase; ATP-binding; Cell division; Cell wall;

Reptidoglycan synthesis; Complete proteome.

108 114 ATP (POTENTIAL).
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                                   STRAIN=ATCC 12228;
PubMed=12950922;
SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                  Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.; "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rrnB-dnaB region.";
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                                                                                                                   Query Match 64.6%; Score 1470; DB 1; Length 436; Best Local Similarity 64.7%; Pred. No. 1.3e-89; Matches 279; Conservative 58; Mismatches 94; Indels (
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2013 (Rel. 42, Last annotation update)
upp-N-acetylmuramete--L-alanine synthetase).
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Peptidoglycan synthesis; Complete proteome.
NP BIND 108 114 ATP (POTEWIIAL).
SEQUENCE 435 AA, 49200 WW; 70C37FCFBCFFAR74 CRC64;
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                                                 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
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MEDLINE=22608415; PubMed=12721630;

MEDLINE=22608415; PubMed=12721630;

Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

Kapatral V., Bortacharyya A., Reznik G., Mikhailova N., Lapidus A.,

Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,

Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,

Overbeek R., Kyrpides N.;

"Genome sequence of Bacillus cereus and comparative analysis with

Bacillus anthracis.";
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FUNCTION: Cell wall formation.
CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine
phosphate + UDP-N-acetylmuramoyl-L-alanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate-_L-alanine ligase (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=226900;
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300

300

360 360 420

240

120 120 180 180

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RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Kobayashi Y., Koetter P., Kohingstein G., Krogh S., Kumano M., Klein C., Kobayashi Y., Koetter P., Kohingstein G., Krogh S., Kumano M., Lavine A., Liu H., Masuda S., Mauler J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Modina M., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M., Parescan E., Pujic P., Purnelle B., Rappoort G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sacotin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takahashi H., Takemaru K., Takahashi H., Takemaru K., Yancuchi M., Tamakoshi A., Storotte R., Socifone F., Vasacuchi M., Tamakoshi A., Tanaka T., Terpatra P., Nambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yanamoto H., Yanane K., Yasumoto K., Yata K., Yoshida K., Yoshida K., Yanamoto H., Yamane K., Yasumoto K., Yata K., Yasumoto B., The Complete genome sequence of the Gram-positive bacterium Bacillus T., Takatills."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Varon D., Brody M.S., Price C.W.; "Bacillus subtilis operon under the dual control of the general stress transcription factor sigma B and the sporulation transcription factor sigma H.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Microbiol. 20:339-350(1996).
-!- FUNCTION: Cell wall formation.
-!- CATALYITC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine = ADP
-!- CATALYITC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanine.
-!- PATHWAY: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the murCDEF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; C69662; C69662.
Subtilist; BG10973; murC.
HAMAP; MF_00046; -; 1.
InterPro; IPR004101; Mur_ligase.
InterPro; IPR004101; Mur_ligase.C.
InterPro; IPR00578; MurC.
Pfam; PF0275; MurLigase.C; 1.
Pfam; PF0275; MurLigase.C; 1.
TIGRFAM8; TIGR01082; murC; 1.
Peptidoglycan synthesis: Cell wall; Cell division; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 114 ATP (POTENTIAL).
432 AA; 48364 MW; B73BF9502FD7CE1B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96310371; PubMed=8733232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z99119; CAB14957.1; -. EMBL; L31845; AAB40043.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 85-432 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=168 / Marburg;
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                                                                                                                                                                                                                                                                                                                                                                          420
61 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120
                                                                  121 HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACBYRRHFLSYKPDYAIMTNIDFDHPDYFK 180
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                               61 GMTVIAGNAFPDTHPEIEKAMSEGIPVIRYHKFLGDYMKKFTSVAVTGAHGKTSTTGLLA
                                                                                    TAFDVYVDGEFYDHFLSPQYGDHTVIMALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
                                                                                                                                                                                                                      241 TTFDVFVRNTFYDTFYIPAYGHHNVLNSLAVIALCHYEEIDSSIIKHALKSFGGVKRRFN
                                                                                                                                                                                                                                                                                       181 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
                                                                                                                                                                                                                                                                      361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 30:3927-3935 (2002).

-i - FUNCTION: Cell wall formation.

-i - CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine = ADP phosphate + UDP-N-acetylmuramoyl-L-alanine.

-i - PATHWAY: Peptidoglycan blosynthesis.

-i - SUNCELLULAR LOCATION: Cytoplasmic (Probable).

-i - SUNLIARITY: Belongs to the murCDEF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
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10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 AA.
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STRAIN=HTE831 / DSM 14371 / JCM 11309;
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR005759; Mur_ligase; 1.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase_C; 1.
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DB 1; Length 432;

63.2%; Score 1438;

Query Match 63.2% Best Local Similarity 64.6% Matches 276; Conservative

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90

1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE

64.6%; Pred. No. 1.6e-87; iive 51; Mismatches 100; Indels φ

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InterPro; IRR000113; Mur_ligase.

InterPro; IRR000101; Mur_ligase_C.

InterPro; IRR000101; Mur_ligase_C.

InterPro; IRR000101; Mur_ligase_C.

Pfam; PF01225; Mur_ligase; 1.

Pfam; PF01225; Mur_ligase; 1.

Pfam; PF01225; Mur_ligase; 1.

Pfam; PF0120875; Mur_ligase; 1.

Pfam; PF0120875; Mur_ligase; 1.

Pfam; PF0120875; Mur_ligase; 1.

Pfam; PF0120875; Mur_C; 1.

Ingase; ATP-binding; Cell division; Cell wall; Peptidoglycan synthesis; Complete proteome.

NP BIND 114

SEQUENCE 433 AA; 48656 MW; ASE6962FCA4760B7 CRC64;
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NCBL_TaxID=1642;
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28-FBB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-DCT-2003 (Rel. 42, Last annotation update)
10-Nacetylmuramate--L-alanine ligase (EC 6.3.2.8)
acetylmuramoyl-L-alanine synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 60.1%; Score 1368; DB 1;
Best Local Similarity 59.3%; Pred. No. 6.6e-83;
Matches 253; Conservative 69; Mismatches 105;
                                                                                                                                                            EMBL; AP001518; BAB06967.1; -. PIR; H84055; H84055.
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MEDLINE=20512582; PubMed=11058132;
Arkami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                1;
                                                                                                                          DB 1; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
                                                                                                                          ; Score 1381.5; DB 1; Length; Pred. No. 8.7e-84; 63; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                     438 AA; 49863 MW; 43AE610786AB1992 CRC64;
       TIGRFAMS; TIGRO1082; murC; 1.
Ligase; ATP-binding; Cell division; Cell wall;
Peptidoglycan synthesis; Complete proteome.
Peptidoglycan synthesis; Complete Proteome.
SEQUENCE 108
APP (POTENTIAL).
SEQUENCE 438 AA; 49863 MW; 43AE610786AB199;
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MURC OR BH3248.
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                                                                                                                            60.7%;
                                                                                                                        Query Match
Best Local Similarity 61.14
Matches 261; Conservative
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SEQUENCE FROM N.A.
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Q9K7W1;
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PIR; AE1275; AE1275.
ListLinst; LW001605; -.
HAMARP; MF 00046; -.; I.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR005758; MurC.
Pfam; PF01225; Mur_ligase_C.
Pfam; PF02875; Murligase, 1.
Pfam; PF02875; Murligase, 1.
IGREPAB; IGR01082; murC; 1.
Ligase; ATP-binding; Cell division; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.0%; Score 1342; DB 1;
59.7%; Pred. No. 3.6e-81;
iive 64; Mismatches 108;
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Peptidoglycan synthesis; Lagra Proteome.
NP BIND 108 114 ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acetylmuramoyl-L-alanine synthetase)
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28-FEB-2003 (Rel. 41, Last seq
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                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Best Local Similarity
                                                                                                                                          OKLONAY 427
                                                                                                                                                                                                         421 OKFOAAY 427
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MURC LISMO
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STRAIN=CLIP 11862 / Serovar 6a;

STRAIN=CLIP 11862 / Serovar 6a;

A Glaser P., Frangeul L., Buchrieber B., Rusnick C., Amend A.,

A Glaser P., Frangeul L., Buchrieber B., Chakraborty T.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Garbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,

A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

A Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

Science 294:849-852 (2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Cell wall formation.
-!- CATALITIC ACTIVITY: AIP + UDP-Nacetylmuramoyl + L-alanine = ADP
-!- Dhosphate + UDP-N-acetylmuramoyl-L-alanine.
-!- PATHWAX: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the murCDEF family.
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR000713; Mur_ligase_C.
InterPro; IPR005758; Mur_ligase_C.
Pfam; PF02875; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase_C; 1.
IIGRPAMS; TIGR.0002; MurC; 1.
Ingase; ATP-binding; Cell division; Cell wall; Peptidoglycan synthesis; Complete protecome.
NP_BIND 108 114 ATP (POTENTIAL).
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ListiList; LIN01646; -.
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Best Local Similarity 60.24
Matches 257; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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361 LADEVYLCDIPGSAREKTGNLTIADLAHKTKGNHIIKEEHTEELLQYPEAVILFMGAGDV 420
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MEDLINE=21537279; PubMed=11679669;

MEDLINE=21537279; PubMed=11679669;

MEDLINE=21537279; PubMed=11679669;

MEDLINE=21537279; PubMed=11679669;

MEDLINE=21537279; PubMed=11679669;

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

Brian K.-D., Fshih H., Garcia-del Portillo F., Garcia D.,

Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Johnsons L.-W., Kaerst U., Kreft J., Kihh M., Kunst F., Kurapkat G.,

Madueno B., Maitournam A., Mata Vicente J., Ng E., Nacipari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Dlaz J.-C., Purcell R.,

Remmel B., Rose M., Schlubeter T., Simose N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

Comparative Pertidoglycan blosynthesis.

Comparative Rock M., Porplasmic (Probable).

Science 294:849-852(2001).

Comparative Rock M., Rock M., Welland F., Chanine.

Comparative Genomics of Listeria species.";

Comparative Genom
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10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
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                                                                                                                                                                                                                                182 INDVFDAFQEMAHNVKKGIIAWGDDEHLRKIBADVPIYYYGFKDSDDIYAQNIQITDKGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 SFEVKYHDESLGKFRIPLFGEHNVINSTAVIAVSYFEKVNLDEIRRELLDFSGVKRRFSB
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weissenbach J., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcu
lactis spp. 111403.";
Genome Res. 11:731-753(2001).
-i- FUNCTION: Cell wall formation.
-i- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine = ADP
                                                                                                                                                                                        Gaps
                                                                                                                                                                                        1;
                                                                                                                                                              DB 1; Length 436;
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16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
                                                                                                                                                              56.5%; Score 1284.5; DB 1; Length
55.7%; Pred. No. 2.1e-77;
ive 75; Mismatches 115; Indels
                                                                                                                                    25A582D850238CD4 CRC64;
       EMBL, AL935256; CAD63921.1; -.
HAWAP; MF 00046; -; 1.
Interbro; IPR0004101; Mur_ligase.
Interbro; IPR004101; Mur_ligase.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase C; 1.
Ligase, ATP-binding; Cell_division; Cell wall; Leptidoglycan synthesis; Complete proteome.
NP_BIND 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 AA
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MEDLINE=21235186; PubMed=11337471;
                                                                                                                                    436 AA; 48750 MW;
                                                                                                                                                             Query Match
Best Local Similarity 55.7%;
Matches 240; Conservative
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QKYEKIYEDQM 435
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                                                                                                                                    SEQUENCE
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MURC LACLA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                 STRAIN=SSI-1 / Serotype M3;
MEDLINE=22683278; PubMed=12799345;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Handada S.,
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
"Genome sequence of an m3 strain invasive strains and new insights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
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                                                                                           SEQUENCE FROM N.A.
STRAIN=MGAS15 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
MEDLINE=22133808; PubMed=12122206;
MEBERS S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 442;
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Streptococcus pyogenes (serotype M3).
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
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NP BIND 109 115 ATP (POTENTIAL)
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InterPro; IPR000713; Mur_ligase..
InterPro; IPR000713; Mur_ligase_C.
InterPro; IPR005758; MurC.
Pfam; PF0225; Mur_ligase_C; 1.
Pfam; PF022875; Mur_ligase_C; 1.
TIGRPAM9; TIGR01082; murC; 1.
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                                                         NCBI_TaxID=198466
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                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DIVXIAQIYGSAREVDHHEITAQDLADKVRKPAKVIDLDNVSPLLDHDRGVYVFMGAGNI
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28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
UDP-N-acetylmuramante-L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramcyl-L-alanine synthetase).
MURC OR SPYM3_0252 OR SPS1607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.9%; Score 1180; DB 1; Length 4
52.7%; Pred. No. 1.6e-70;
ive 79; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 AA; 50050 MW; ABEDAB52E9638C8A CRC64;
                                                                                                                                                                                                                                                               HAMAR, MUNICOLOGIO, 1. 1.

InterPro; IPR000713; Mur_ligase.

InterPro; IPR004013; Mur_ligase.

R Pfam; PP01225; Mur_ligase; 1.

R Pfam; PF02875; Mur_ligase; 1.

R IGRRAMs; TIGR01082; mur_l.

W Ligase; ATP-binding; Cell division; Cell wall;

W Ligase; ATP-binding; Cell division; Cell wall;

Peptidoglycan synthesis; Complete protecome.

R Peptidoglycan synthesis; Complete protecome.
                       -!- PATHWAY: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the murCDEF family.
     phosphate + UDP-N-acetylmuramoyl-L-alanine
                                                                                                                                                                                                                                                     EMBL; AE006433; AAK06138.1; ALT_INIT.
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Best Local Similarity 52.74
Matches 227; Conservative
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QKYELAF-EKL 434
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ID MURC_STRP3
AC Q8K8Ū5;
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                                                                                                               304 IANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKAD 363
                                                                                                                                                                                364 RVFLCEIFGSIRE-NTGALTIQDLIDK-IEGASLINEDSINVLEQFDNAVILFMGAGDIQ 421
                                                                                                                                                                                                  244 DVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETT 303
                                                                   245 KVKHQGEVIGQEHVPAYGKHNILNATAVIANLEVAGIDMALVADHLKTFSGVKRRFTEKI 304
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Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Liyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Oian Y., Jia H.G., Najar F.Z., McLaughlin R.;
Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
-!-FUNCTION: Cell wall formation.
-!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine = ADP +
                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-Pr-AcceryImuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphate + UDP-N-acetylmuramoyl-L-alanine.
-- PATHWAY: Peptidoglycan blosynthemia.
-- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-- SIMILARITY: Belongs to the murCDEF family.
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                                                                                                                                                                                                                                                                                                                                                                 442 AA
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STRAIN=SF370 / ATCC 700294 / Serotype M1;
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR000713; Mur_ligase_C.
InterPro; IPR005758; MurC.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase_C; 1.
TGRFAMB; TIGR01082; mur_ligase_C; 1.
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микс ок spY0345.
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Q9A1C7;
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Length 442;

50.1%; Score 1139; DB 1;

Query Match

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                                                                                                                                                124 NGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MGAS8232 / Serotype M18;
STRAIN=MGAS8232 / Serotype M18;
MEDLINE=21927593; PubMed=11917108;
MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Syva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Rapur V., Daly J.A., Veasy L.G., Musser J.M.,
Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks.";
                                                4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
                                                                        64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM
                                                                                                                                                                                                                        DVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGTAF
                                                                                                                                                                                                                                                                                                  244 DVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETT
                                                                                                                                                                                                                                                                                                                                                                          245 KVKHQGEVIGQEHVPAYGKHNILNATAVIANLEVAGIDMALVADHLKTESGVKRRFTEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
-!- FUNCTION: Cell wall formation.
-!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine = ADP
                 2; Gaps
50.7%; Pred. No. 7.9e-68; ive 82; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramete--L-alanine ligase (EC 6.3.2.8)
acetylmuramoyl-L-alanine synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphate + UDP-N-acetylmuramoyl-L-alanine.
-!- PATHWAY: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the murCDEF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 LYEHSFEELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=186103;
 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MURC STRP8
                                                                                                                                                                                                                                                                                    184
     Best Loca
Matches
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CC modified and this statement is not removed. Usage by and for commercial correct entities requires a license agreement (See http://www.isb-sib.ch/announce/ cc rend an email to license@isb-sib.ch).

CC C EMBL; AE009982; AAL97144.1; -.

DR HAMAP; MF 000466; -; 1.

DR InterPro; IPR000713; Mur_ligase.

DR InterPro; IPR0013; Mur_ligase.

DR InterPro; IPR00140; Mur_ligase.

DR Fdam; PF01225; Mur_ligase.

DR Ffam; PF02075; Mur_ligase.

CR InterPro; IPR001082; murC; 1.

DR Ffam; PF02075; Mur_ligase.

CR InterPro; IPR01082; murC; 1.

DR Ffam; PF02075; Mur_ligase.

CR InterPro; IPR01082; murC; 1.

DR Ffam; PF02075; Mur_ligase.

CR InterPro; IPR01082; murC; 1.

DR Ffam; PF02075; Mur_ligase.

CR InterPro; IPR01082; murC; 1.

DR Ffam; PF02075; Mur_ligase.

CR InterPro; IPR01082; murC; 1.

CR
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Query Match
49.9%; Score 1135; DB 1; Length 442;
Best Local Similarity 50.5%; Pred. No. 1.5e-67;
Matches 217; Conservative 82; Mismatches 129; Indel8

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422 KLONAYLDKL 431 ::::: | 425 LYEHSFEELL 434 Search completed: June 3, 2004, 14:39:38 Job time: 19 secs

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DATA COS CONTRA 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7w4b5 bordetella
Q7wuq4 bordetella
Q87wy6 pseudomonas
Q817 coxiella bu
Q82v82 nitrosomona
Q7v3p8 prochloroco
                                                                                                        June 3, 2004, 14:36:31; Search time 46 Seconds (without alignments) 2997.423 Million cell updates/sec
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                                                                                                                                                                                                                 1 MTHYHFVGIKGSGMSSLAQI.....GDIQKLQNAYLDKLGMKNAF 437
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Q88WZ5
Q8DY77
Q8E3U2
Q8DSP4
Q899J1
Q9RNM7
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Q7WFS3
Q7WFB5
Q7WUQ4
Q87WY6
Q83F17
Q82VS2
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sp_mammal:*
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sp_vertebrate:*
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sp_organelle:*
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seq length: 200000000
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sp_rodent:*
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Sp_human:*
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Q7vejl prochloroco	Derark remopulation	O83mf8 shidella fl			_		Q821s4 chlamydophi	_				m					Q7vqi7 candidatus		Q8ph24 xanthomonas		Q83gnl tropheryma				Q9jue5 neisseria		Q8eyr2 leptospir	
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17	18	61	2 6	4 0	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	9	4	41	42	43	44	45	

ALIGNMENTS

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RESULT 1

(983306)

CHANGE OF GENERATORY; PRT; 445 AR.

DG 083306

DT 01-JUN-2003 (TEFMBLRel. 24, Last sequence update)

DT 01-JUN-2003 (TEFMBLRel. 25, Last sequence update)

DE 01-JUN-2003 (TEFMBLRel. 25, Last sequence update)

DE 01-JUN-2003 (TEFMBLRel. 25, Last sequence update)

NE 02 Excercis Faccoccus faccals (Streptococcus faccals).

NE 02 Excercis Faccoccus Excercis faccals (Streptococcus faccals).

RESURENCE TROWN N. Mers 6. N. Wers 6. N. Heidelberg J.F.,

RA Paulsen I.T., Baneriel L., Wers G. N., Heidelberg J.F.,

RA Paulsen I.T., Baneriel L., Wers G. N., RA Read T.D., Fordson R. J., Umayam L., Brinken J., Rabaran M.,

RA Paulsen I.T., Baneriel L., Werchum R. A., Goldonay J., Kitouri H.,

RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Kitouri H.,

RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Kitouri H.,

RA Vamathevan J., Tran B., "Upton J., Hansen T., Shetty J., Kitouri H.,

RA Vamathevan J., Predlis N., "Intervolution of vancomycin-resistant

Excisence 299:2011-2074(2003).

RESULE CONTROL OF STATP binding; IEA.

DR GO: GO:0005524; F.AIP binding; IEA.

DR GO: GO:000553; P.E.Dopmuramate-L.-alanine ligase activity; IEA.

DR GO: GO:000553; P.E.Dopmuramate-L.-alanine ligase.

DR InterPo: IPRO04013 Mur. ligase.

DR InterPo: IRRO04013 Mur. ligase.

DR InterPo: IRRO04082; Mur. ligase.

DR INTERPO: IRRO04082; Mur. ligase.
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us-10-712-713-2.rspt

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Ligase; Complete proteome.
SEQUENCE 436 AA; 48750 MW; 25A582D850238CD4 CRC64;
                                                                                     Best_Local Similarity 55.7%
Matches 240; Conservative
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A Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
A Kleerebezem M., Boekhorst J., van Kranenburg R., Sandbrink H.M.,
A Fiers M.W.B.J., Stlekema W., Klein Lankhorst R.M., Bron P.A.,
A Hoffer S.W.B.J., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
De Vos W.M., Slezen R.J.;
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
RMBL, AL93526; CAD63921.1;
"R GO; GO:0005524; F:ATP binding; IEA.
R GO; GO:000958; F:Igase activity; IEA.
R GO; GO:0009058; P:Diosynthesis; IEA.
R GO; GO:0009058; P:Diosynthesis; IEA.
R InterPro; IPR004101; Mur_ligase.C.
R InterPro; IPR004101; Mur_ligase.C.
R Pfam; PF0225; Mur_ligase.C; 1.
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                                                                  DB 16; Length 445;
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                            86; Indels
                       445 AA; 49999 MW; 12189004F4FBIE9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
UDP-N-acetylmuramate-alamine ligase (EC 6.3.2.8).
                                                               63.2%; Score 1438.5; DB 60.9%; Pred. No. 1.2e-92;
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STRAIN-NCIMB 8826 / WCFS1;
    Ligase; Complete proteome
                                                                                                                 Matches 259; Conservative
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                                                                    Query Match
Best Local Similarity
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                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                      182 INDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 ADRVFLCEIFGSIRENTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDI
                                                                                                                                                                                                                                                                                                                     122 VANGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKD
                                                                                                       2 THYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKED
                                                                                                                                                                                                              62 MVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH
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                                                      Gaps
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  DB 16; Length 436;
                                                      1;
56.5%; Score 1284.5; DB 16; Lengt
55.7%; Pred. No. 7.6e-82;
ive 75; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
UDP-N-acetylmuramate--alanine ligase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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MEDLINE=22222988; PubMed=12200547;
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GO:0005840; C:ribosome; IEA.
GO:0005840; C:ribosome; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0016874; F:Idgage activity; IEA.
GO:00018735; F:structural constituent of ribosome; IEA.
GO:0008763; F:UDP-N-acetylmuramate-L-alanine ligase activity; IEA.
GO:000973; P:biosynthesis; IEA.
GO:000973; P:coll wall biosynthesis (sensu Bacteria); IEA.
GO:0006412; P:protein biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 MNGDKKTSFLIGDGTGWGLPESDYFAFEACEYRRHPLSYKDDYAIMTNIDFDHPDYFKDI
: |||||||||| : ||||||| :
125 LKNITDTSFLIGDGTGRGSANANYFVFEADBYERHFMPYHPEYSIITNIDFDHPDYFTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 YHFIGIKGSGMSALALMALHQMGHNVQGSDVDKXYFTQRGLEQAGVTILPFSPNNISEDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 NDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 VIQGNAF-ASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 TIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKA
                     Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.7%; Score 1153.5; DB 16; Length 443; 51.0%; Pred. No. 1.2e-72; rative 82; Mismatches 126; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBDSP4;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative UDP-N-acetyl muramate-alanine ligase (EC 6.3.2.8)
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                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00936; RIBOSOMAL L35; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 443 AA; 49836 MW; 0BDBD0CDE
                                                                                                                                                                                                                                                             Interpro; IPR005758; MurC;
Interpro; IPR000713; Mur ligase.
Interpro; IPR004101; Mur ligase C.
Interpro; IPR001706; Ribosomal L35.
Pfam; PP0225; Mur ligase; 1.
Pfam; PP02875; Mur ligase C; 1.
TIGRPAMS; TIGR01082; murC; 1.
                                    invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002)
EMBL; AL766852; CAD47323.1; -.
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RGO; GO:0016974; F:ligase activity; IEA.

GO; GO:003735; F:structural constituent of ribosome; IEA.

GO; GO:0009763; F:uDP-N-acetylmuramate-L-alanine ligase activity; IEA.

RGO; GO:0009058; P:biosynthesis; IEA.

GO; GO:0009273; P:cell wall biosynthesis; IEA.

RO; GO:0006412; P:procein biosynthesis; IEA.

RILEEPER; IPROGO713; Mur.ligase.

RILEEPER; IPROGO713; Mur.ligase.

RILEEPER; IPROGO713; Mur.ligase.

RILEEPER; REGO106; Ribosomal_E35.

REGEN; PFO1225; Mur.ligase.

RIGREAMS; TIGRO1082; mur.c; 1.

REGEN; PROSTIE; PSO0936; RIBOSOMAL_L35; 1.

ROSTIE; PSO0936; RIBOSOMAL_L35; 1.

ROSTIE; PSO0936; RIBOSOMAL_L35; 1.

ROSTIE; PSO0936; RIBOSOMAL_L35; 1.

ROSTIE; PSO0936; RIBOSOMAL_L35; 1.
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SEQUENCE FROM N.A.
STRAIN=NEMBL6 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                   5 YHFIGIKGSGMSALALMLHQMGHNVQGSDVDKXYFTQRGLEQAGVTILPFSPNNISEDLE
                                                                                                                                                                                                                                                                                                                                                                                                4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
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                                                                                                                                                                                                                                                                                                                         Length 443;
                                                                                                                                                                                                                                                                                                                       51.1%; Score 1163.5; DB 16; Lengt
51.3%; Pred. No. 2.4e-73;
cive 81; Mismatches 120; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Last annotation update)
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AGDIQLYERSFEELL 435
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                                                                                                                                                                                                                                                                                                                                                               223; Conservative
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                                                                                                                                                                                                                                                                                                                                          Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 RIQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKI--EGASLIN----EDS 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 ADHLDYYKDINHIKNAFSKFANLIPKDGYLIACAEDBNINDIIKNIDCTIITYGL-NKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 HFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFDANNIKEDMV
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                                                                                                                                                                      Clostridium tetani.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The genome sequence of Clostridium tetani, the causative agent
                                                                                                                                                                                                                                                                                                                                                                                                                                        Brueggemann H., Baeumer S., Frické W.F., Wiezer A., Liesegang
Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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27.8%; Score 633.5; DB 16; Length
Best Local Similarity 35.1%; Pred. No. 3.8e-36;
Matches 158; Conservative 91; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456 AA; 50816 MW; 31C71A197188CBB5 CRC64;
                  01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDYLKKETKPGDLVLIMGAGDIYKAGDLFL 455
Created)
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01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Massachusetts / E88;
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SEQUENCE 456 AA; 50816
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=1513;
                         01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                               Clostridium
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REMBL, AEG15001, ANAUS9364.1; -...

RG GO; GO:0005840; C:ribosome; IEA.

GO; GO:0005524; F:AFP binding; IEA.

GO; GO:0005524; F:AFP binding; IEA.

GO; GO:0005735; F:Igase activity; IEA.

GO; GO:0009735; F:Structural constituent of ribosome; IEA.

GO; GO:0009735; F:UDP-N-acetylumuramate-L-alanine ligase activity; IEA.

GO; GO:0009735; F:cell wall biosynthesis (sensu Bacteria); IEA.

GO; GO:0009735; P:cell wall biosynthesis; IEA.

RO; GO:0006412; P:protein biosynthesis; IEA.

RI CO; GO:0006412; P:protein biosynthesis; IEA.

RI InterPro; IPR001705; Ribosomal Ligase.

RI InterPro; IPR001706; Ribosomal Liss.

REMI, PF0125; War ligase; 1.

REMI, PF0125; War ligase; 1.

REMI, PF0125; War ligase; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IQGNAFASSHE-EIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGDKKTSFLIGDGTGMGLPESDYFAFFACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDIN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 RVFLCEIFGSIRE-NTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDIQ 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74
                                                                                                                                                                   MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UA159, a cariogenic dental
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                                                                                                                                                                                                                                                                                                                                                    pathogen.";
Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002)
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                                    NCBI_TaxID=1309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||: ::| |||: | :: | |||: | 393 SRIKDLYDDFVEVLSQVDCLILLDVYSAGEAPVPGADSRALCRSIRQ------RQQLDP 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 MVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 AQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRIQAFLNEFAESLSKADRVFLCEIFG------SIRENTGALTIQDLIDK 389
                                                                                                                                                                                 Ishii A., Nakasone K., Sato T., Sugai M., Wachi M., Nagai K., Kato C., "Isolation and characterization of dcw gene cluster for cell division and cell wall synthesis from a deep-sea piezophilic Shewanella violacea.";
                                                                                                                                                                                                                                                                                    EMBL; AB052554; BAB19203.1; -. GO; GO:0005737; C:cytoplasm; IEA. GO; GO:0005737; C:cytoplasm; IEA. GO; GO:0005524; F:ATP binding; IEA. GO; GO:0016874; F:ligase activity; IEA. GO; GO:0000763; F:blosyntheeis; IEA. GO; GO:0009058; P:blosyntheeis; IEA. GO; GO:00273; P:cell wall biosyntheesis (sensu Bacteria); IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 PD-YFKDINDVFDAFQEMAHNVK-KGI-IAMGDDEHLRKIEADV--PIYYYGFKDSDDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 HIYFVGIGGAGAGGAAEVLVNBGYRLSGSDIAENAVTE-RLKSLGVQIHIGHHADQVHGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 HYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFDANNIKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 TFGGVKRRFNE----TTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTF
                                              Shewanella violacea.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 494;
                                                                                                                                                                                                                                                                      Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01225; Mur_ligase; l. —
Pfam; PF02875; Mur_ligase C; l.
TIGREAM; TIGR01082; murC; merC; SEQUENCE 494 Aa; 54098 MW; 96E45B6A503E48E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Murc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.0%; Score 523.5; DB 2; Best Local Similarity 31.8%; Pred. No. 2.2e-28; Matches 145; Conservative 88; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 IEGASLINEDSINVLEOF--DNAVILFMGAGDIOKL
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR005758; Murc.
InterPro, IPR000713; Mur_ligase.
InterPro, IPR004101; Mur_ligase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                       SEQUENCE FROM N.A.
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Q8E9P8;
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                                                                                                                                                                                                                                              130 LDAGGIDPTVINGGIINSY----GSNARLGDSDWMYVEADESDGSFLRLDGTLAIVINID 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 VVVVSSAIHRGNPEVEAALENRIPVVRRAEMLAELMRLKSTVAVAGTHGKTTTTSMVAAL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 ADIRAVDITPISGGNRFTAVIRGRDGDIRRIENIFLPMPGRHNIQNALSAIGVALEFSIP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 VAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEG---- 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 IAVVOPHRFLRLHDLMTEFQSAFNDADMVFVAPVYAAGEOPIAGVDSGALVSGLKQHGHR 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 HFVGIGGIGMSGIAEVMHNLGYQVQGSDISEGY--TVDALRQMGIKVLIGHHAENVKDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 FDHPDYFKDINDVFDAFQEMAHNVKKGIIAWGDDEH-----LRKIEADVPIYYYGFKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDIYAQNIQITDKGTAFDVYV---DGEF--YDHFLSPQYGDHTVLNALAVIAISYLEKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 VTNIKEALETFGGVKRRFN---ETTI--ANQVIVDDYAHHPREISATIETARKKYPHKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 HFVGIKGSGMSSLAQIMHDLGHEVQGSDI~ENYVFTEVALRNKGIKIL-PFDANNIKEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Zymomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.6%; Score 536.5; DB 2; Length 486; 32.5%; Pred. No. 2.7e-29; ative 75; Mismatches 174; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ASLINEDSINVLEQFDNAVILFMGAGDIQK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486 AA; 52602 MW; 7DB255E70F47CCD4 CRC64;
                01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) UDP-N-acetylmuramate-alanine ligase.
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                           STRAIN=ZM4;
Um H.W., Kang H.S.;
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                                                                                              Zymomonas mobilis.
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=542;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIQAFLNEFAESLSKADRVFLCEIFGS-----IRENTGALTIQDLIDKIEGAS--L 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 M-NGDKKISFLIGD-----GIGMGLPESDYFAFEACEYRRHFLSYKPDYAIMINIDFDHP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D-YFKDINDVFDAFQEMAHNVK-KGI-IAWGDDEHLRKIEADVP--IYYYGFKDSDDIYA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKGALET 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 YGQAGRDPTFVIGGLINSAGTNARLGTSRYLIAEADESDASFLHLQPMVSVVTNIEADHM 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 HFVGIGGAGMGGIAEVIVNEGYVVSGSDIAQNAVTDRLCL--LGAKIHIGHGADNVQQAD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 HFVGIKGSGMSSLAQIMHDLGHEVQGSDI-ENYVFTEVALRNKGIKI-LPFDANNIKEDM 62
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GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:000876; F:DP-N-acetylmuramate-L-alanine ligase activity; IEA.
GO; GO:0009058; F:Db:Osynthesis; IEA.
GO; GO:0009273; P:cell wall biosynthesis (sensu Bacteria); IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Gell J., Uterback T.R., McDonald L.A., Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gabs
                 MURC OR SO4218.
Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488 AA; 53168 MW; DC45914D4869D353 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.9%; Score 521.5; DB 32.6%; Pred. No. 3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INEDSINVLEOFDNAVILFMGAGDIOKL
UDP-N-acetylmuramate--alanine ligase
                                                                                                                                                                                                                                                                                                                             Mat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015855; AAN57190.1; -.
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
                                                                                                                               STÄÄIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
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Pfam, PF02875, Mur ligase C; 1.
TIGRFAMS, TIGR01082, murC; 1.
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Best Local Similarity
                                                                                                                SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=70863;
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SEQUENCE FROM N.A.

STRAIN=RBSO / ATCC BAA-588;

CATAIN=RBSO / ATCC BAA-588;

MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

A Harris D.E., Holden M.TG., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A Achtman M., Akin R., Baker S., Basham D., Bason N., Cherevach I.,

A Achtman M., Akin R., Hamlin M., Cronin A., Dayle F. Doggett J.,

Relication A., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Minin L., Whitehead S., Barrell B.G., Maskell D.J.;

Comparative analysis of the genome sequences of Bordetella pertussis,

Rabinowitsch E., Mother Schools.

Rabinowitsch S., Sander S., Sander S., Squares K.,

St. Mat. Genet. 35:32-40(2003).

EMBL; Bx64049; CAR145011; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 MDTYGHDVARLKSARIBFTQRLPFYGSAILCADDANVREIMPFYSRPITTYGLSPDAQVC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 AQDVQA -- DGTRWRFTVQRRDRDVVLPALQVELNLPGLHNVRNALAAIAVATELGVDDAA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 MVVIQGNAFASSHERIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 HYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFDANNIKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 468;
                                                                                                                                                                                                         MURC OR BB4197.
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.3%; Score 506.5; DB 16; Length 31.7%; Pred. No. 3.2e-27; .ive 75; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. 468 AA; 49404 MW; 045E233D594FECFD CRC64;
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                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8).
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PRT;
                                                                                                                                                                                                                                                                                                        Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 31.7
Matches 145; Conservative
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=518;
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468 AA.

PRT;

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PRELIMINARY;
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Barris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quall M.A.,

Achtman M., Akrin R., Baker S., Basham D., Bason N., Cherevach I.,

Achtman M., Akrin R., Baker S., Basham D., Bason N., Cherevach I.,

Achtman M., Akrin R., Baker S., Basham D., Bason N., Cherevach I.,

Achtwell T., Goble A., Hamlin N., Hauser H., Hollroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmond M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

Nat. Genet. 35:32-40(2003).

In Nat. Genet. 35:32-40(2003).

EMBL, BaK640434; CAR39034:1; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 PD-YFKDINDVFDAFQEMAHNVK--KGIIAWGDDEHLRKIEADV--PIYYYGFKDSDDIY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 VVAVFQPHTFSRTQAFLNEFASLSKADRVFLCEIFGS------IRENTGALTIQDL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 MVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAIVTSTAVAGDNPEVLAARAARIPVVPRAVMLAELMRLKRGIAVAGTHGKTTTTSLVAS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 IREALAAFKGVGRRFTQWGDLPVPAAHGGGTFTLVDDYGHHPVEMAATLAAARGAWPQRR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 HYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFDANNIKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                            Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.3%; Score 506.5; DB 16; Length 31.7%; Pred. No. 3.2e-27; Artive 75; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          468 AA; 49404 MW; 045E233D594FECFD CRC64;
                                                                                                      01-07T-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
UDP-N-acetylmuramate--alamine ligase (EC 6.3.2.8).
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                                                         468 AA
                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=12822 / ATCC BAA-587;
MEDLINE=22827954; PubMed=12910271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 145; Conservative
                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                     BPP3751.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=519;
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                                                                                  Q7W4B5;
  RESULT 11
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RESULT 12

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Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
A Achtman M., Akkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Monberczak H., O'Neil S., Ormond D., Price C.,
Rabbinowitsch E., Rutter S., Sanders D., Seeger K.,
Sharp S., Simmond M., Skelton J., Squares R., Squares S., Stevens K.,
Munkin L., Whitchead S., Barrell B.G., Maskell D.J.,
Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
RMAL, Genet. 35:32-40(2003).
REMBL, EXE4020; CAE43293.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 IREALAAFKGVGRRFTQWGDLPVPAAHGGGIFTLVDDYGHHPVEMAATLAAARGAWPQRR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 VVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGS-----IRENTGALTIQDL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 GAIVTSTÄVÄGDNPEVLAÄRAARIPVVPRAVMLABLMRLKRGIÄVÄGTHÖKTTTTSLVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 VM-NGDKKTSFLIGD-----GTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 PD-YFKDINDVFDAFQEMAHNVK--KGIIAWGDDEHLRKIEADV--PIYYYGFKDSDDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 MDTYGHDVARLKSAFIEFTQRLPFYGSAILCADDANVREIMPFVSRPITTYGLSPDAQVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                              Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.3%; Score 506.5; DB 16; Length 468; Best Local Similarity 31.7%; Pred. No. 3.2e-27; Matches 145; Conservative 75; Mismatches 195; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 AA; 49416 MW; 1E77233D4366E724 CRC64;
01-077-2003 (TrEMBLrel. 25, Created)
01-077-2003 (TrEMBLrel. 25, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8).
MURC OR BF3022.
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=TOhama I / ATCC BAA-589 / NCTC 13251;
MEDLINE=22827954; PubMed=12910271;
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SEQUENCE 468 AA; 49416 N
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                                                                                                                                                                Bordetella pertussis.
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Q87WY6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 M-NGDKKTSFLIGD-----GTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDH- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 FAAGGLDPTFVIGGRINAAGTNAQLGTSRYLIAEADESDASFLHLQPLVAVVTNIDADHM 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231
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Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Uterback T., Van Aken S., Feldblyum T., Gwinn M.,
Berry K., Uterback T., Van Aken S., Feldblyum T., Gwinn M.,
A bodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.,
White O., Fraser C., Collmer A.,
The Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

IL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

IN TIGR, PSFTO4407; -.
RO, GO:0005524; F:ATP binding; IEA.
RO, GO:000554; F:ATP binding; IEA.
RO, GO:0005874; F:ATP binding; IEA.
RO, GO:000588; P:Diosynthesis; IEA.
RICEPTO: IPRO0410; Mur_ligase.
RICEPTO: IPRO0410; Mur_ligase.
RICEPTO: IPRO0410; Mur_ligase.
RICEPTO: March Policy March Policy Mur_ligase.
RICEPTO: March Policy Mur_ligase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 HFVGIGGVGMCGIAEVILINLGYEVSGSDLKGSAVTE-RLESFGAQIFVGHRAENTVGADV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 PDYFKDINDVFDAFQEMAHNVK-KGI-IAWGDDEHLRKIEADV--PIYYYGFKDSDDIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TFGGVKRRF---NETTI--ANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
                                                                                                                                                                         Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 486;
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22.1%; Score 502; DB 16; Length 4:
Best Local Similarity 33.1%; Pred. No. 7e-27;
Matches 154; Conservative 80; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 AA; 52671 MW; 9020894E5F27C757 CRC64;
      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
MUP-N-accetylmuramate--alanine ligase.
MURC OR PSPTO4407.
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Pfam; PF02875; Mur ligase C; 1.
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STRAIN=DC3000;
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174 DH-PDYFKDINDVFDAF-QEMAHNVKKGIIAWG-DDEHLRKIEADVP--IYYYGFKDSDD 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 AQYRVVDYCQQG-----IQSLFQIH--SPQRKAPLIVKLSMPGQHNALNAIAVTAIADV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: ::| || || || || || 297 VQMNEPALLKSLADFPGVDRRF---TIRGEMILPKGNALIIEDYGHHPNEIKATLAAARA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 SHV-MNGDKKTSFLIG----DGTGMGLPESDYFAFEACEYRRHFLSYKEDYAIMTNIDF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GDHTVLNALAVIAISYL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDIQKLQNAYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0009763; F:UP-N-acetylmuramate-L-alanine ligase activity; IEA.
GO; GO:00099058; P:biosyntheeis; IEA.
GO; GO:0009273; P:cell wall biosyntheeis (sensu Bacteria); IEA.
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REDILINE=22608657; PubMed=12704222;

Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,

Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,

Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Dodson R.J.,

Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,

Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;

"Complete genome sequence of the Q-fever pathogen, Coxtella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78;
                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Coxiellaceae; Coxiella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.0%; Score 500; DB 16; Length 4. 29.5%; Pred. No. 9e-27; rative 86; Mismatches 177; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) UDP-N-acetylmuramate--alanine ligase.
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EMBL; A2016960; AA089700.1; -.
TIGR; CBU0136; -.
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR004013; Mur_ligase..
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase C; 1.
IIGRFAMS; TIGR01082; murc; 1.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016874; F:Ingase activity; IEA.
GO; GO:0008763; F:UDP-N-acetynuramate-L-alanine ligase activity; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
GO; GO:000273; P:cell wall biosynthesis (sensu Bacteria); IEA.
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Murc; UDP-N-acetylmuramate--alanine ligase protein (EC 6.3.2.8)
MURC OR NE0992.
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Nitrosomonadaceae, Nitrosomonas.
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462 QTHG 465
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	. !	AX742069 Sequence	1274	1703	AX617936 Sequence	5134	APOUSSES SCADINATOC	AFORTON STADIO	AX191741 Semience	E35613 Murc. 6/200	BD178030 Murc. 4/2	AE016748 Staphyloc	E35614 Murc. 6/200	BD178031 Murc. 4/2	AE017039 Bacillus	AEUL/UIS BACILLUS	Sequence	Oceanob	Listeri	Sequenc	AX413017 Sequence	AL591979 Listeria	AX641669 Sequence	AFOORSSO BACITLUS BU	AP001518 Bacillus	AE006433 Lactococc	AX607160 Sequence	AE014265 Streptoco	AASUZIJO SEQUENCE	AL/86852 Streptoco	AE01414 Streptoco	AP005146 Streptoco	AE009982 Streptoco	AL935256 Lactobaci	Taleds Baciling cu	AE008507 Streptoco	AX569902 Sequence	7447	7 7 7	AL449927 Streptoco			linear PAT 10-MAY-2003				واسموس إبطعها	J. LOCOCCER .	, Awrey, D.,	Kanagarajah, D., Nethery, K., inder B. Viola C. and		
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Corganism="Staphylococcus aureus"
/mol type="genomic DNA"
/db_xref="taxon:1280"
Novel purified polypeptides involved in
Patent: WO 03025007-A 27 27-MAR-2003;
Affinium Pharmaceuticals Inc. (CA)
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Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and Rosen, C.A.
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RESULT 3

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99.5%; Score 1311; DB 6; Length 1332;
Best Local Similarity 100.0%; Pred. No. 1.6e-189;
Matches 1311; Conservative 0; Mismatches 0; Indels 0
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Sequence 899 from Patent W002094868.
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Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I., Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Lian, J., Ito, T., Kanamori, M., Matsumaru, H., Maruyama, A., Murakami, H., Hosoyama, A., Karahashi, N.K., Sawano, T., Inoue, R., Kaito, C., Sekimizu, K., Hirakawa, H., Kuhara, S., Goto, S., Yabuzaki, J., Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C., Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hiramatsu, K., Whole, genome sequencing of metatitain-resistant Staphylococcus
                                                                                    1222 ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTATTATATGGGTGCAGGTGATATT 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-JAN-2001) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; Zhome 49-10 Nighihara, Shibuya-ku, Tokyo 151-0066, Japan Center; Zhome 49-10 Nighihara, Shibuya-ku, Tokyo 151-0066, Japan Tel:ali-3-3481-1933- Pass. 181-3-3481-8424) On Jun 12, 2001 this sequence version replaced gi:13701258.

Location/Qualifiers
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Hosoyama,A. Magai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H.
Direct Submitssion
Submitted (30-JAN-2001) Director-General, Biotechnology Center
National Institute of Technology and Evaluation, Biotechnology

    .301550
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                                                                                                                                                                       1282 CAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTT 1332
                                                                                                                                      1261 CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTT 1311
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Pafvilssgfgkdeqrseqtyqvavalelihwatlvhddvidksdkrrgkliskkwd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SAS045"
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/complement(7777. .8226)
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/product="heptaprenyl diphosphate syntase component II"
/protein_id="BAB42563.1"
(db_xref=-ig1:13701269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="ORFID:SA1301"
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/cransi_table=1:
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/protein_id="BAB42562.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (7368. ,7568)
/gene="SA1300"
/note="ORFID:SA1300"
/codon start=1
/transl_table=11
                                                     QHIDQTTLQHACEQLKTYFK"
complement (5816, .6982)
                                                                                                          /gene="aroC"
complement(5816. .6982)
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/gene="SA1300"
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                                                                                                                                                             /gene="aroC"
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Gaps

Query Match
99.5%; Score 1310.8; DB 1; Length 301550;
Best Local Similarity 99.8%; Pred. No. 3.5e-190;
Matches 1312; Conservative 0; Mismatches 2; Indels 0; G

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291118 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC 291059
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                                                                                                               ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA
                                                                                                                                                                                                                              GTTGCTCTTAGAAATAAGGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAAA
                                                                                                                                                                                                                                                                                                                                                GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA
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KVINKSETPPFSINEENVNVDENKYRLDGEFYALPQSPQLAGTFKORHQITRSIRQYLD
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HUPFTSPKRAADIAACGTAPERSARANYDIVLNGYELGGGGSIRIHDGELQEKMFEVLGF
TKEQAQEGFELLDAFKYGAPPHGGIALGRILVMLTYRRTNLRDTIAPPKYTASATCI
LTNAAGEVSDKQLEELSLRIRH"
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LVINSVGDMASRKEYNEALVKHFEPVIHEPCSDCQSRLHTNPMRILDCKVDRDKEALY
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DGAITTLCGGGRYNGLLELLDGPSFTGIGFALSIERLLLALEEEGIELDIEBNLDLFI
VTMGDQADRYAYVGLIMLENNGIKADKDYLQRKIKGQMKQADRLGAKFTIVIGDQELE
NNKIDVKNMTTGESETIELDALVEYFKK"
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STDLFARGVGDSTDVVQKEMYTFKDKGDRSITLRPEGTAAVVRSYIEHKWQGNPNQPI
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NLDIVADNYKEKNPLOGKTIVLDPGHGGSDOGASSWYKYKSLEKDYTLKTAKELCRTL
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DTLDATIOKKGLLSKRGSROENYQVLRQTKVPAVLLELGYISNPTDETWIKDCLHRQI
LEQAIVDGLKIYFSA"
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                                                                                                                                                                                                                                      /translation="MGFLAAYTPYMKDVQNKKQGTHLXITGRMIKLL"
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/gene="hiss"
/note="SAV1631"
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complement(1276. .3042)
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/gene="hiss"
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complement (5654. .6106)
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transl_table=11
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/transl_table=11
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/note="SAV1632"
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290038 AAAGCAGATGTGTATTCTTATGTGAATTTTTGGATCAATTAGAGAAAATACTGGCGCA 289979
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On May 29, 2001 this sequence version replaced gi:13875943.
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Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Lian, J., Ito, T., Kanamori, M.,
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Sekimizu, K., Hirakawa, H., Kuhara, S., Goto, S., Yabuzaki, J.,
Kanehisa, M., Yamashita, A., Ogime, K., Furuya, K., Yoshino, C.,
Shiba, T., Hattori, M., Ogasawa, Hayashi, H. and Hiramatsu, K.
Whole genome sequencing of meticilla resistant Staphylococcus
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                                                                                                                                                                                            AP003363 342600 bp DNA linear BCT 24-APR.
Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete
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/strain="Mu50"
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Staphylococcus aureus subsp. aureus Mu50
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complement (1029. .1130)
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/db_xref="taxon:158878"
complement (42. .815)
/gene="SAV1628"
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complement(1029, .1130)
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/gene="SAV1628"
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EIRTSKHSYGPSRAMMIKIVKSSSAKGKIKSFFKKQDRSSNIEKGRAMVEVEIREQGFIV
VEDILIFKNIQVVNEKYNFANEDDLFAAVGFGGVTSLQIVNKLITERQRILDKQRALNE
EQUTKELIPKDNIITUSGVYVEGENYTGLGIVNKLITERQRILDKQRALNE
TÜCENIKNETERLINTENGANGANGKYQVDLEVTAYDRNGILNEGGGTKVHR
TÜCENIKNETERLINTSVANVNDVYRVVEKIKQLGDVYTVTRVMN"
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                                                                                                                                                                                                                                                                                                                                                                                                                               KONGLPYIMHPIQVAGILJEMRLDGPTIVAGFLHDVIEDTPYTFEDVKEMFNESVARIV
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IRISRETLETYAPLAHHIGINTIKWELEDTALRYIDNYOYPRIVMKKRESERRAYI
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KIYEYFNDALRAYGLTVKTGEFGTHMNVSINNDGPVTIIYESQDGKIQ"
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                                 complement (6118. .8307)
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                                                                       /gene="relA"
complement(6118.
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note="SAV1635"
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                                                                                                                      132799 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC
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                                                                                                                                                                                                                                                                  GTTGCTCTTAGAAATAAAGGGGGATAAAAAAATATTACCATTTGATGCTAATAAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                         TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA
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                                                                                 IGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC
                                                                                                                                                           ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA
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                                             Gaps
        1; Length 342600;
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    Score 1310.8; DB 1
Pred. No. 3.3e-190;
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  99.5%;
                    Similarity 99.8
2; Conservative
Query Match
Best Local Simi:
Matches 1312; (
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YYGEKOSDDIYAQNIQITDKGTAFDYVVDGEFYDHFLSFQYGDHTVLNALAVIAISY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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ERYVGDSSLNDDSDLTDNSTDASQLHTNGIENETVSNDENKQASIQNEDTNDTHVDES
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BEDGATNKEEYSGSQIDDAEFYELINDTEADEDTTSNIEDNTNRNASEMHVDAPKTQEH
AVTESQYNIN IDKTVDNEIELAPRHKKODQTNILNVNSLKTNDNDGHYVBDSSRNBIEK
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EVSDITEESSETTHPNNTSGQQDNDDQQKDLQPSFSNQNEDTANENRPRTNQQDVATN
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QVYEGPSVTRRELSVBKGYVSRITALDDDINGALAAKDI RIBALIPGTSVGVGIEVDN
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VCINSILMSLLYKNHPBELRILLIDPKAVBLAPINGLPHLVAPVITDVKAATQSIKWA
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RIQGKARGGIHMLYATQBENVNITELIKANIPTRIAFARNSSVDERTILDSGABER
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QSQDELFDDVCAFMVNEGHISTSLIQRHFQIGYNRAARIIDQLEQLGYVSSANGSKPR
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                                                                                                                                                                                                            lypothetical protein, similar to general stress protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon gtart=1
/transl_table=11
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                                                                  complement (1907. .2398)
                                                                                                                        complement (1907. .2398)
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/note="ORFID:MW1683"
                                                                                                                                                                           note="ORFID: MW1682
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/note="ORFID:MW1685
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/transl_table=
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1201 ATTAATGTATTAGAACAATTIGATAATGCTGTTATTTTTTATGGGTGCAGGTGATATT 1260
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QQAAIKEEVSANNLSDTSQEAQEIQEAKKEAQAETDKSAAVSNEESKAAALKAQQAAI
KEEASANNLSDTSQEAQEIQEAKKEAQAETDKSAAVSNEESKAAALKAQQAAIKEEAS
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QKQAKLTPGSKESQLTEALFAEKPVAKNDLKEIPQLVTKKNDVSESETVNIDNKDTVK
QKEAKFENGVITRKADEKTTNNTAVDKKSGKQSKKTTPSNKRNASKASTNKTSGQKKQ
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Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and
Kikuchi,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (106-WAR-2002) Director-General, Biotechnology Center,
Submitted (106-WAR-2002) Director-General, Biotechnology
Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mali-bioGenite-go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1333, Fax:81-3-3481-8424)
Location/Qualifiers
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Genome and virulence determinants of high virulence
                                                                                                                                                                                                                                             AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
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AP004828 BAR000033
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/organism="Staphylococcus aureus subsp. aureus MW2"
/mol_type="genomic DNA"
/strain="MW2"
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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/transl_table=11
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INAIVAKYEDKKEKIVDEIVYYUDALAQMADKTLESISSSOLMPVIRATSFDKKTKO
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db_xref="GI:21204859"

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ASSGMICSKKELNIPAAPEEKGIMVLNDSYEIGQAFFE"
complement (8279. .9136)
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/boxtein_id="01:21204857"

/translation="WKQLESEQFESIKQGATVPEFTAGWCPDCRVIEPDLPELEARY

pmpDpvSvDRDKFMDICIENGIMGIPSFLVYKNGELLGSYIGKERKSIEQIDAFLAQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /iote="ORFID:MM1688
and-1,4-beta-glucanase homolog"
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phenylalanyl-tRNA synthetase (beta subunit) homolog"
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/protein_id="BAB95551.1"
/db_xref="G1:21204856"
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complement(11211. .12053)
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10775. .11086
/gene="MW1689"
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                                                                                                                                                      Gaps
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0
                                                                                             Score 1309.2; DB 1; Length
Pred. No. 6.2e-190;
0; Mismatches 3; Indels
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/transl_table=11
/product="conserved hypothetical protein"
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Score 1302.8; DB 1;
Pred. No. 2.8e-188;
0; Mismatches 7;
                98.8%;
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             Query Match
Best Local Similarity
Matches 1307; Conserv
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ELKLDVTNIKGALEFFGGYKRRENETTIANQYIVDYAHFREISATIETARKYPHK
ELVDVAVPQPHTFSRTQARINETASLSKADRVFLCEIFGSIRENTGLLTIQDLIDKIEG
ASLINDEDSINVLEQFDNAVVLFKGAGDIQKLQNAYLDKLGMRARF"
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2 (Dases 1 to 1314)

Lowe, A.M. and Deresiewicz, R.L.

Direct Submission

Direct Submission

Submitted (11-NOV-1997) Channing Laboratory, Brigham and Women's

Hospital and Harvard Medical School, 181 Longwood Ave, Boston, MA

02115, USA
                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus UDP-N-acetylmuramoyl-L-alanine synthetase (murc) gene, complete cds.
AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
                                                                                                        AAAGCAGATCGTGTATTCTTATGTGAAATTTTTTGGATCAATTAGAAAAAATACTGGCGCA
                                                                                                                                           ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTTTATGGGTGCAGGTGATATT
                                                       CAACCACACTITCTCTAGAACACAAGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT
                                                                                                                                                                                                                        ATTAATGTATTAGAACAATTTGATAATGCTGTTGTTTTATTATGGGTGCAGGTGATATT
                                        CAACCACACTTTCTCTGTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT
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/note="MurC; UDP-N-acetylmuramate-alanine ligame"
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
I (bases I to 131)
Lowe, A.m. and Deresiewicz, R.L.
Cloning and sequencing of Staphylococcus aureus messential for cell wall biosynthesis
DNA Seq. 10 (1), 19-23 (1999)
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/organism="Staphylococcus
/mol_type="genomic DNA"
/db_xref="taxon:1280"
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Antisense antibacterial/cell division composition and method Patent: WO 0149775-A 23 12-JUL-2001;
Avi Biopharma, Inc. (U$)
Location/Qualifiers
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98.8%; Score 1302.8; DB 6; Length 1314;
Best Local Similarity 99.5%; Pred. No. 2.8e-188;
Matches 1307; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                          linear
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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/organism="Staphylococcus a
/mol_type="unassigned DNA".
/db_xref="taxon:\280".
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Sequence 23 from Patent
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15-OCT-2002
25-DEC-2001 JP 2001391079
03-JUL-1997 US 60/052720
NICOLA G WALLIS,MARTIN K R BURNHAM
C12N15/09,AGIK31/7088,AGIK38/43,AGIK38/55,AGIK45/00,AGIK48/00,
AGIP1/00,
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Patent: JP 2002300888-A 1 15-OCT-2002;
SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM PLC
OS Unidentified
PN JP 200330088-A/1
PP 15-OCT-2002
PP 15-OCT-2002
PP 25-DEC-2001 JP 2001391079
PR 03-JUL-1997 US 60/052720
PR NTCOLA G WALLLS, MARTIN K R BURNHAM
PC CL2N15/09, A61K31/7088, A61K38/55, A6:
PC A61P1/00,
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Wallis, N.G. and Burnham, M.K.R.
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                                                                                          L MITHILINE BEECHAM CORP, SMITHKLINE BEECHAM CORP PUBLIC LTD CO
SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM CORP PUBLIC LTD CO
S Unidentified
PN 1999225773-A/1
PD 24-AUG-1999
PF 03-JUL-1998 UP 1998225115
PR 03-JUL-1999 UP 1998225115
PC C12N15/09, A61K31/70, A61K38/53, A61K39/085, A61K39/395,
PC A61K48/00, A61K48/00, C07K16/40, C12N1/21, C12P21/02, C12P21/08, PC
C12Q1/68,
PC G10X13/566//(C12N15/09, C12R1:445), (C12N1/21, C12R1:445), PC
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    1. 1351
    /organism='Unidentified'

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                                                                                                                                                                                                                                                                                                          PC G01N33/566//(C12N15/09,C12R1:445)
C12N15/00,A61K37/60,
PC A61K37/64,(C12N15/00,C12R1:445)
CC Strandedness: Double;
CC Topology: Linear;
FH Key
FT Source Losalinear;
FT FOURCE CONDICTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                           1 (bases 1 to 1351)
Nicola,G.W. and Martin,K.R.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
35613
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Staphylococcus epidermidis ATCC 12228, section 5 of 9 of the ADD16748 ABD16748 ABD16748 ABD16748 ADD16748 ADD16
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Staphylococcus epidermidis ATCC 12228
Bacteria; Firmicutes; Bacillales; Staphylococcus.

Expectia; Firmicutes; Bacillales; Staphylococcus.

Expectia; Firmicutes; Bacillales; Staphylococcus.

Expectia; Firmicutes; Bacillales; Staphylococcus.

In (Aman, Z., Chen, Z., and Wen, Y., Qin, Z., Chen, Z., and Wen, Y., Qin, Z., Chen, Z., and Wen, Y., Chinese National Human Genome Center at Shanghai, Z. 540 Bi Bo Road, Shanghai, 201203, China

Location Qualifiers

In 1300029

| Corganism=Estaphylococcus epidermidis ATCC 12228"
| Amol_type="genomic DNA" |
| Strain="ATCC 12228" |
| Ab xref="ATCC: 12228" |
| Complement(137. 1123) |
| Co
GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA
                                                                                                                                                                GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA
                                                                                                                                                                                                                                                                           GATGTTACAAATATTAAAAGCATTAGAAACGTTTTGGTGGTGTTAAAACGTCGTTTCAAT
                                                                                                                                                                                                                                                                                                                      862 GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGATTAAACGTCGTTTCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                        GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1081 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1162 TTAACGATACAAGATTTAATTGATAAATTGGAGGTGCATCGTTCATTAATGAAGATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1282 CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1335
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/protein_id="AA004767.1"
/db_xref="GI:27315632"
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/locus tag="SE1168"
/codon_start=1
/transl_table=11
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PC A61P7/02,A61P9/00,A61P11/00,A61P13/02,A61P13/12,A61P17/00, PC A61P19/02, A61P19/02,A61P19/02,A61P21/00,A61P25/00,A61P27/00,A61P29/00, PC A61P39/02,A61P43/00,C07K14/195,C12N1/15,C12N1/19,C12N1/21, PC C12N5/10, PC C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,C12N15/00, PC A61K37/48,A61K37/64

CC MurC Location/Qualifiers

FF Rey Location/Qualifiers

FT source Location/Qualifiers

FT source Location/Qualifiers

FT source Location/Qualifiers
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/organism='Unidentified'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1293.2; DB 6 Pred. No. 7.8e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .1351
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/ETAINSTALLINGTONE-WANGLUSVVIKLMLTILLIVATVLILLSVSLITFIQYYFTQETEN
AIKBDARKISSLYRKTHALONSQTLILDSOPGGGLIIMKOMSEKEDSSYKOTKKO
MFNEIKKSTKEYKKVPKEGEYETQNITIKKNANSQSYLLLGYPWKAQKRAQSHYSGVFI
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YKOLKSIEDTYNNALTIILILTAIIFTIASTIFAFEKSNYIRDTLLNSWVEGVLGINNQ
RETILSKYADDINKHIDDPEKESIEQDIRATPESQNRYLELEINTRYYYPISSYID
RIQTNGRSGIVWYIRDMTNEHNLOQMKOFIANVSHEIRTPISLLOGYTESIVOLSYR
ROSELGLITMTFDSNNDEQLWNYDMDRADQVLTNLIDNATRYTQAGDSIKISIDEDSD
FNILLITTDTGTGTAR DEBLIKQVPDRFYKVDAARKRGKQGTGLGIFICKMIIEEHGGRID
VBSELGKTFFIRLPKSQYGIS"

COMDIEMENT (8766. .9491)

// LOCUE LAGE LAGE 182176"
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complement (10355. 10897)
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nnyaciildim.pemdgibyasklrehkdppiimltakgeennyegebsgaddyivk
pepervultaktphykalikrtqpnntegsephardiiefshlyidndahkvladdqqvult
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SLIYGLITGTIVMTILLSILMYFYLLDLYGDPYRFNLIND
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/product="staphylococcal respiratory response protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="staphylococcal respiratory response protein
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'product="hypothetical pr
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complement (7016, .8782)
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                   / translation: "MISTANDED PERNAGER REPRENTAGE INPOEQCY ELKEDDKT NEW KKEADS QNSLSNNSNOOPPRAGER REPRATATNOS KQODKHQKNSDAKTTEG SLDDRYDBAQLOQQHDKS QQODKHQKNSDAKTTEG SLDDRYDBAQLOQQHDKS QQODKHQKNS BADDRYBKUGGRAAI VNGTSES PERHENKSKSTON RECPKAQQOKKRSSTOSKESTOSKES TYDDRYAATGAGIAGAAGVAGAAGVAGABES REHHNKKDKQD SKHSNHENDEKS VKNDDQKQS KKGKKAATGAGIAGAAGVAGAAGVAHHNNQNKHHNEEKNS NQNNQYNVDSSEKKKGFPKILLPLIALILICAIAI FEGGMALNHNDSKSDDQKTAN QSKCDSDKKDGAQSEDNKDKKSDSNKDKKSDSDKNDAAGVAGAAGVAHNNONKHNDGYLVIPQ"
ANNNSNYTWQNQODRANQNSNNQATQSQSHTVYGGENLYRIAIQYYGEGTQANVDK IKRANGLSSNNIHNGQTLVIPQ"
COMDIE menet (2795. . 4174)
/locus tag="SE1170"
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TVTKITDKSVTYEKDGQLIEIDNDYVFAMIGYHPDYDFLKTIGIDIHTNEYGTAPVYN
RETPETNVENCYIAGVIAAGNDANTIFIENGKYHGGVITQSILTKKQTPLET"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / LTAIN BALTON = "MAGONLKEWPGPDEFKEGGEEIIDSVLHGRHTLGILPTGSGKSL
CYQLPTYLIEKPTLISPLISAMDDOWGTKAKGETHVACHSGMDEVERDNIKRLS
KSRFIYLSPEYILQPHOFTAINFOLLVUDEAHCLSEWGYDPRPHYALVGKTIHHF
NSATVLALTATARS POPENDEAHLISLKANVOKSMNRENISLGHYNFNDDEGKTEWLL
PPLSNSGPTIIYOSKKRCLELAQMIYDSSYLLGITHGDLSYQERQTVQQQFRNNDIP
VLATSARGMGINKKDIFTVIHHTLSSSPSNTLOGIGHAGDLSYQERQTVQQQFRNNDIP
VLATSARGMGINKKDIFTVIHHTLSSSPSNTLOGIGHAGDLSYQERQTVQQQFRNNDIP
ILETLLETDLFTDIITDDDITMEFTGNHLDPEKEKLISTIANGPFFSGLKDIFFORDSR
ILETLLETDLFTDIITDDDITMEFTGNHLDPEKEKLISTIANGPFFSGLKDIFFORDSR
GYMRNMGYTNLDDGCRRKYLLEFFGEHPQSPKQCCEQDSRLEPIQILNRKKVKRKLSFN
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INNKFAITTTKGVYBCKYLTVATGYYGQHNTLEAEGAELPKVFHYFKEAHPYFNQNVV
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complement (4161, .5123)
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complement (5572. .5676)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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5232. .5480
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CDS

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E 1 (Dages 1 to 660)

S Nicola,G.W. and Martin,K.R.B.

Murcola,G.W. and Martin,K.R.B.

Authorities becchan CORP, SMITHKLINE BEECHAM CORP PUBLIC LTD CO

SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM CORP PUBLIC LTD CO

OS Unidentified

PD 24-AUG-1999

PP 03-JUL-1999 US 60/052720

PR 03-JUL-1999 US 60/052720
247865 TATGGCTTTAAAGAAACAGATGACATCTATGCTAAAAATATTCAAATTACTGAAAAGGT
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                                                                                                                    247805 ACGCAATTTGATGTATATTAAAGGCGAATTTTATGATCAATTCTTATCCCCACAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247505 CAACCACATACGTTCTCAAGAACTCAAGCATTTTAAACGAATTTGCTGAGAGTTTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247445 AAGGCAGACCAAGTATTTTTATGTGAAATATTCGGTTCAATAAGAGAAAATACGGGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247385 TTAACTATAGAAGATTTAATCGAATCGTATTGACGGCTCGACGCTTATAGATGAAATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTECTITIGALGIGATGIGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT
                                                                                                                                                                       781 GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA
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                                                                                                                                                                                                                                                                                                                      247685 AATGTAGAAAATATTAAAGAAGCACTGATAACATTTGGTGGTGTAAAACGTCGTTTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTECTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT
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                                                                                                                                                                                                                                                                                                                                                                      GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCACCATCCAAGAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314
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C12N15/00,A61K37/60,
PC A61K37/64,(C12N15/00,C12R1:445)
CC Strandedness: Double;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                      /codon_start=1
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EMIRGINSDGAVKTLIARGLVEAKDVDHSRSHHLITTDLFLNVFGIENLDALPTTEED
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                                                     producT="conserved hypothetical protein"
protein id="AA004777.1"
/db_xref="GI:27315642"
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                                                                                                                                                                                                 EARMDEFFSNLVNOKGESNE"
complement (10890. 11690)
/locus_tag="SE1179"
complement (10890. 11690)
/locus_tag="SE1179"
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541 IGTATTAGAACAATTTGATAATGCTGTTGTTTTATTTATGGGTGCAGGTGATATTCAAAA
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                                                                                                                                                                                                                                                                                                                             /organism="unidentified"
/mol_type="genomic DNA"
/db xref="taxon:32644"
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                                                                                                                                          48.4%; Score 637.8; DB 6; Length 660;
98.9%; Pred. No. 2.3e-87;
ive 0; Mismatches 7; Indels 0
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/organism='Unidentified'.
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/organism="unidentified"
/mol_type="genomic DNA"
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Wallis, N.G. and Burnham, M.K.R.
Murc
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BD178031.1 GI:30015295
JP 200230088-A/2.
unidentified
 Topology: Linear,
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Best Local Similarity 98.9
Matches 642; Conservative
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Patent: JP 2002300888-A 2 15-OCT-2002;
SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM PLC
OS Unidentified
DN 19 2002300888-A/2
PD 15-OCT-2002
PP 25-DEC-2001 JP 2001391079
PR 03-JUL-1997 US 60/052720
PR NICOLA G WALLIS, MARTIN K R BURNHAM
PC C12N15/09, AGIX31/7088, AGIX38/43, AGIX48/00, AGIX48/00,
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A61P39/02,A61P43/00,C07K14/195,C12N1/15,C12N1/19,C12N1/21, PC
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Location/Qualifiers
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VERSION KEYWORDS SOURCE

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Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzapple, E.,
Okstad, O., Helgason, E., Rilefone, J., Mu, M., Kolonay, J., Beanan, M.,
Dodson, R., Brinkac, L., Gwinn, M., DeBoy, R., Madup, R., Daugherty, S.,
Burkin, A., Haft, D., Nelson, W., Peterson, J., Pop, M., Khouri, H.,
Radune, D., Benton, J., Mahamoud, Y., Jiang, L., Hance, I., Weidman, J.,
Berry, K., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A.,
Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I., Nelson, K., Tettelin, H., Foute, D., Eisen, J., Gill, S., Holtzapple, E., Okstad, O., Helgason, E., Rilefone, C., Wu, M., Kolonay, J., Beanan, M., Dodson, R., Brinkac, L., Gwimn, M., DeBoy, R., Madupu, R., Daugherty, S., Radune, D., Benton, J., Mahamoud, Y., Jiang, L., Hance, I., Weidman, J., Berry, K., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A., Thomason, R., Redmond, C., Thowaite, J., White, O., Salzberg, S., Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and
                                                                                                                                                                                                                      BCT 30-APR-2003
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Yafrdrrokkrdfrkunitrinaaarmnglsysrlmhglknagievnrkmladiavhd
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria
Nature 423 (6935), 81-86 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (26-MAR-2003) The Institute for Genomic Research, 9712
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note="identified by match to PFAM protein family HMM
                                                                                                                                                                                                                AE017039 291804 bp DNA linear BCT 30-AFF
Bacillus anthracis str. Ames section 16 of 18 of the complete
                      ATTACAAAATGCATATTTAGATAAATTAGGCATGAAAATGCGTTTTAA 1314
                                                601 ATTACAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA
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mol_type="genomic DNA"
strain="Ames"
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Location/Qualifiers
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AE017039 AE016879
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PID:1805280, PID:537331, PID:829111, and PID:836669;
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complement(1632. .3569)
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/locus_tag="BA4819"
complement(735. .1295)
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103051 CTTCATGACATGAAGCATACTGTTCAAGGGTCTGATTATGAAAAGCGTTTCTTTACACAA 102992
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VTTSMIERSIVKLYEYIGQSVGCADCPDLGSCKNMLGGYEPKLVIQGKMIDIQYDRCV
RKVAYDERKYEKLVGSVYMPTDILQATMENDDEDSDLDARIDAIGAANEFLSAYEPGK
KVQGIYLYGKFGVGKTVLLGALANEDARKKISSMLYYPEFFIREIKSIQDNSIGEKI
DAVKRVQVLMLDDIGAEAMSSFVRDDVLGALIQFRMIENDFFFTSNFDFKQLEHHLT
YTQRGEAEEWKAARIMERIKYLAKPIPIGGKRNRHK"
YKLEQEYQMFIETLRQQVRSRKSRLSCVHLIFDESFIFYDDKGRRLKQEKLYRYMDED
LLKQKDVYIDTKVIAPLLSISPKKIYLYTKEQDHNMIITLRNVFQERVQLHGLHBFER
NVKNLKNKGNALDFLSF"
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SFNDVFGSFNPGQLEHAQEDLRIPKTTAMPSNEKGDAPKVWNDFFDFSLFVDGLSALV
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GQALFVIJERVQPHAARVMKEKEPSTQEEMI I KQLEEI SPKQLIKEI SGGAEATKADL
GU EDVUMI NYKLIPGVVNVI I YYVMLASDMKIAKTYVBKI AGHWARKKYGTVBRAMAL
AKEENROYOGWAETKKKGRI SKKTVRKEMVPDMIKEEPKEQEKETVKKDASAEKGAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEKQSWMELLPIDRYKVSAKGLLHNYDRKVLTMLYQPLIGSRAF
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ELRDIDDVAYVRFASVYRQFKDLNVFIEELKOILQKERE"
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                                                                                                                       /locus tag="BA4822"
/note="gimilar to GB:X57110, GB:X69207, SP:P22681,
PID:29731, GB:X57110, GB:X69207, SP:P22681, and
PID:29731; identified by sequence similarity; putative"
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/transl_table=11
/product="DNA replication protein Dna8"
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/locus tag="BA4824"
/note="identified by match
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/trans1_table=11
/product="ATP cone domain
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Pred. No. 4.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAP28512.1"
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complement(6010. .7416)
/gene="dnaB"
                                             complement (5038. .5976)
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complement(8291..8683)
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                                                           102991 ACAGCGTTGGAAAAGCGTAATATCTCGATTCTTCCTTTTGATAAAAGTAATGTAAAAGAA
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                                                                                                                             GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA
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101911 ACGGATGTATTAAAGAAACATAAAAAGCGCGTTCTCATTTTCATGGGCGCAGGAGACATC 101852
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OLIGO NUC Scoring table:

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3373863 seqs, 2124099041 residues Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

	Description	Aas00189 S. aureus	Add15462		Add15464	Aca19726	Aas54558 Staphyloc	Aas51660	Aav99650	Aav74703 Staphyloc	Aav80065	Aav53479	Aas50351 Staphyloc	Acal7633 Prokaryot	Aas49022 Staphyloc	Aas49054	Aa849060	AaB48994	Aca16308	Aca16221 Prokaryot	_	Aca16261 Prokaryot	Aas48839	
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ALIGNMENTS

RESULT 1 AAS00189

AAS00189 standard; DNA; 1318 BP.

AAS00189;

(first entry) 04-JUL-2001 S. aureus DNA encoding UDP-N-acetylmuramate:L-alanine ligase, MurC.

UDP-N-acetylmuramate:L-alanine ligase; MurC; immunogen; vaccine; antibody; wound infection; cellulitis; burn infection; eyelid infection; food poisoning; joint infection; meonatal conjunctivitis; osteomyelitis; skin infection; scalded skin syndrome; toxic epidermal necrosis; Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis;

Staphylococcus aureus.

Location/Qualifiers "Murc" /product= 1. .1314 /*tag= a

WO200116292-A2 08-MAR-2001. 31-AUG-2000; 2000WO-US023773.

99US-0151933P. (HUMA-) HUMAN GENOME SCI INC. 01-SEP-1999;

Choi GH;

WPI; 2001-183259/18. P-PSDB; AAU00828 New isolated nucleic acid for use in diagnosing Staphylococcus infections and in vaccines for eliciting immune responses to the infections.

Claim 1; Page 14; 225pp; English.

an The sequence encodes S. aureus MurC (UDP-N-acetylmuramate:L-alanine ligase). The polymucleotides of the invention are used to detect Staphylococcus undeled acids in a blological sample from an animal for diagnosing Staphylococcus infections. The polypeptides of the invention are used to detect anti-Staphylococcus antibodies in a biological sample from an animal to diagnose Staphylococcus infections. The polypeptides are also used in vaccines to elicit protective antibodies in an animal to infection caused by a member of the Staphylococcus genus and for preventing or attenuating an infection, cellulitis, burn infection, eyelid infection, food poisoning, sinfection, neonatal conjunctivitis, osteomyelitis, skin infection, scalded skin syndrome (also known as toxic epidermal necrosis, Ritter's



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disease and Lyell's disease), toxic shock syndrome and endocarditis. The polymucleotides may also be used in vaccines and for preventing or attenuating a Staphylococcus infection. Antibodies to the polypeptides may be used to purify, detect and target the polypeptides in in vitro and in vivo diagnostic and therapeutic methods
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                                                                                                                                                                Query Match 100.0%; Score 1318; Best Local Similarity 100.0%; Pred. No. 0; Matches 1318; Conservative 0; Mismatches
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WPI; 2003-468119/44. P-PSDB; ADD15463

Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria.

Claim 20; SEQ ID NO 27; 325pp; English

This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus), Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (B. coli) that provide novel antimicrobial targets. Specifically, it refers to that provide novel antimicrobial targets. Specifically, it refers to polypeptides that are involved in membrane biosyntheeis, which play a critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate characterisation by labelling with isotopic or heavy atoms, and also characterisation by labelling with isotopic or heavy atoms, and also information to aid the discovery of therapeutic molecules to treat disorders associated with a particular pathogenic species. As such, they care useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for developing antimicrobial agents for use as surface disinfectants, personal hygiene applications and as food preservatives or in treating food products to eliminate potential pathogens. This polymucleotide sequence is DNA predicted from the genomic sequence of S. aureus UDP-N-sectylmuramate-alamine ligase (murc) of the invention.

Sequence 1335 BP; 472 A; 161 C; 255 G; 447 T; 0 U; 0 Other;

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180 240 360 420 480 541 GAIATTAATGATGTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAGGTATT 600 201 261 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA 300 321 381 CATGTTATGATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA 441 501 481 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTTAAA 540 82 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 141 502 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA 561 81 GTTGCTCTTAGAATAAGGGGATAAAATATTACCATTTGATGCTAATAACATAAAAGAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA TATACTICAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA TIGCCIGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT 22 ATGACACACTATCATTTTGTCGCAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAAATATAGACGTCACTTTTTAAGT 1 AIGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC Gaps ö DB 9; Length 1335; Indels ; 0 99.7%; Score 1314; D 100.0%; Pred. No. 0; Live 0; Mismatches Query Match Best Local Similarity 100. Matches 1314; Conservative 361 142 241 301 19 181 202 382 421 442 121 262 322

1020 1200 1260 1080 1221 1281 1101 1161 1041 960 720 741 780 840 861 900 981 801 921 562 GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT ACTGCTTTTGATGTGTGGTGAGGTTTTTATGATCACTTCCTGTCTCCACAATAT GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGGTGGTTAAACGTCTTTCAAT GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCATCCAAGAGAAATT 961 AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT 982 AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT 1021 CAACCACACATTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT 1042 CAACCACACACTTTCTCTAGAACACAGGCATTTTTTAAATGAATTTGCAGAAAGTTTAAAGT 1081 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA 1222 ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTTATTGGGTGCAGGTGATATT CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314 CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAATGCGTTTTAA 1335 682 742 601 1261 1282 661 721 781 802 841 901 922 1102 1201 셤 요 쉽 qq g 쉽 à ö à à 셤 ò 8 g ò 8 셤 ò 셤 셤 Ġ à ò

ACF72770 standard; DNA; 1332 (first entry) 20-NOV-2003 ACF72770 ACF72770 ID ACF7 XX RESULT 3 BXSX EXEX BXSX

Staphylococcus aureus DNA #450

Antibacterial, vaccine; gene therapy, infection; sepsis, diagnosis; enzymatic assay; antibiotic target gene; ds. Staphylococcus aureus

WO200294868-A2 28-NOV-2002

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27-MAR-2002; 2002WO-IB002637. 27-MAR-2001; 2001GB-00007654

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ADD15464 standard; DNA; 1335
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                                                                                                                                                           The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a paramaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus genes of the invention
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                                                                                                                                       Claim 6; SEQ ID NO 899; 49pp; English
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                                                                                         New Staphylococcus aureus
preventing Staphylococcal
S. aureus, e.g. sepsis.
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                                                         WPI; 2003-120786/11.
            CHIRON SPA
                                                                   P-PSDB; ABM71210
                                 Masignani V,
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622 ATTGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT 681
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                                                                                                     TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATCAAATTACGGATAAAGGT
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                                                                                                                                                                                 <u>ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT</u>
                                                                                                                                                                                                                                                                                                      GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA
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1. .1335
/*tag= a
/product= "MurC protein"
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PF 20-SEP-2002; 2002WO-CAGUIT28-XX
21-SEP-2001; 2001US-0323992P.
PR 21-SEP-2001; 2001US-0324152P.
PR 25-SEP-2001; 2001US-0324692P.
PR 26-OCT-2001; 2001US-033924P.
PR 30-OCT-2001; 2001US-0340924P.
PR 30-OCT-2001; 2001US-0340924P.
PR 18-DEC-2001; 2001US-0341332P.
PR 18-DEC-2001; 2001US-034173P.
PR 19-DEC-2001; 2001US-034173P.
PR 19-DEC-2001; 2001US-034177P.

(AFFI-) AFFINIUM PHARM INC.

Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B; Domagala M, Houseon S, Kanagarajah D, Nethery K, Ng I, Mansoury K; Mcdonald M, Pinder B, Viola C, Wrezel O;

WPI; 2003-468119/44. P-PSDB; ADD15465. Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria.

Claim 20; SEQ ID NO 29; 325pp; English

This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus), Streptococcus premoniae (S. preumoniae) and Escherichia coli (E. coli) that provide novel antimicrobial targets. Specifically, it refers to polypeptides that are involved in membrane biosynthesis, which play a critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate characterisation by labelling with isotopic or heavy atoms, and also characterisation by labelling with isotopic or heavy atoms, and also information to aid the discovery of therapeutic molecules to treat disorders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for devaloping antimicrobial agents for use as surface disinfectants, personal hygiene applications and as food preservatives or in treating conducts to eliminate potential pathogens. This polymucleotide sequence is the experimentally predicted DNA of S. aureus UDP-N-acetylmuramate-alanine ligase (murc) of the invention.

Sequence 1335 BP; 472 A; 160 C; 255 G; 448 T; 0 U; 0 Other;

120 141 GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA 180 201 240 261 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTTAGGACAGATTATTGATCAA 300 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA 321 9 8 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA Argentarian de la companica della companica della companica della companica de GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA 1 ATGACACATATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC 22 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTTCATTAGCACAAATC Gaps .. DB 9; Length 1335; 1; Indels Score 1263; DB Fred. No. 0; Mismatches Query Match
Best Local Similarity 99.9%;
Matches 1313; Conservative 82 121 142 181 241 à g ð d 8 셤 à d

à	301	
q ₀	322	TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAACTTCTACAACAGGTTTATTATCA 381
λō	361	
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λζ	421	TIGCCUGAAAGUGAITAITITCGCITITGAGGCAIGIGAATAIAGACGICACITITIAAGI 480
Op	442	S
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qa	502	TATAAACCIGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA 561
λõ	541	GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGGCACATAATGTTAAAAAAGGTATT 600
Dp	562	GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT 621
à	601	ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT 660
ДQ	622	ATTGCTTGGGGTGATGAACATTTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT 681
ò	661	TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT 720
Db	682	TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT 741
à	721	ACTGCTTTTGANGTGTAATGTGGANGGTTGAGATCACTTCCTGTCTCCCACAATAT 780
Dp	742	ACTECTITICATGLETATGTGGATGATGTTTTATGATCACTICCTGTCTCCCACAATAT 801
à	781	GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA 840
qq	802	GGTGACCATACAGITITIAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA 861
à	841	GAIGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT 900
qq	862	GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT 921
λζ	901	GABACTACAATIGCAAATCAAGTTATIGTAGATGATTATGCACACCATCCAAGAAATT 960
ДD	922	GAAACTACAATTGCAAATCAAGTTATTGTAGATTATGCACCACCATCCAAGAGAAATT 981
λŏ	961	961 AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT 1020
qq	982	AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT 1041
ζ	1021	CAACCACACACTITCTCTAGAACACAGGCATTITTAAATGAATTTGCAGAAAGTTTAAGT 1080
Db	1042	CAACCACACTITCTCTAGAACACACATITTTAATGAATTTGCAGAAAGTTTAAGT 1101
ογ	1081	AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA 1140
QQ	1102	AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA 1161
λō	1141	TTAACGATACAAGATTTAATTGATAAAATTGAAGGGCGCATCGTTAATTAA
qq	1162	TTAACGATACAAGATTTAATTGATAAATTGAAGGTGCATCGTTAATTAA
à	1201	ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTATTTA
qq	1222	ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTATTTA
č	1261	CAAAAATTACAAAATGCATATTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314
qq	œ	133

KESULI S ACA19726 ID ACA19726 standard; DNA; 1314 BP

ds; prokaryotic essential gene; cell proliferation; Prokaryotic essential gene #1383 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-0CT-2001; 2001US-0342933P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 (first entry) (ELIT-) ELITRA PHARM INC. Staphylococcus aureus drug design; gene WO200277183-A2 19-JUN-2003 Antisense; ACA19726

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C. Malone Zamudio C, Trawick JD; WPI; 2003-029926/02 P-PSDB; ABU15856. ų, Wang

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 7596; 1766pp; English.

the invention fraints to am instance acts comprising any one or the invention fraints to am its invention fraints to an interaction of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated continued for proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying proteins or screening for homologous nucleic acids are useful for clantifying proteins or screening for homologous nucleic acids required for interaction and organism. The antisense modeled acids required for clandidate modeled acids are useful for clandidate and descreen and acids are useful for clandidate and all and provery more are not for generalized modeled acids are useful for clandidate and all and provery more are not for erreaning and when a provery more and a provery more and acids are useful for an area of the strains or for erreaning and acids are useful for an area of the strains and and an area of the acids required for a provery more an organism. drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at five wipo.int/pub/published_pct_sequences one of invention relates to an isolated nucleic acid comprising any

Sequence 1314 BP; 464 A; 161 C; 250 G; 439 T; 0 U; 0 Other;

Length 1314;

92.0%; Score 1212; DB 7;

Query Match

ö 1020 120 1080 120 180 240 240 300 300 360 420 420 480 480 540 540 009 900 099 999 720 720 780 780 840 840 900 096 9 900 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA CATCAATTGAAATTAGATGTTGTATAAATGATTTTTTTAGGACAGATTATTGATCAA 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA GTTGCTCTTAGAAATAAGGGGATAAAATATTACCATTTGATGCTAATAACATAAAAAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA TATACTICAGIAGCIGIAACIGGIGCACAIGGIAAAACTICIACAACAGGITIAITAICA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA 481 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTTAAA Argacacacraritaricaricasaarraaagerrcregecarcagraritageacacaaare 361 CALGITATGAATGGTGATAAAAAGACTICATITITAATIGGTGATGGCACAGGTATGGGA CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT TIGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTAAGT 421 TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT ATTGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCCACAATAT GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA CAACCACACTTTCTCTAGAACACAGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT GATGTTACAAATATTAAAGGAATTAGAAACGTTTGGTGGTGTTAAAACGTCGTTTCAAT GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCACCATCCAAGAAAATT GAAACTACAAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT Gaps AGTGCTACAATTGAAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT ; 2; Indels 0; Mismatches Pred. No. 99.88; Matches 1312; Conservative Best Local Similarity 61 121 121 181 241 241 301 301 601 196 196 1021 361 421 481 541 541 199 661 721 721 781 781 841 901 901 d Š 셤 ਨੋ 셤 ਨੇ g 셤 à 셤 à à g à g Вþ ਨੇ à g à g ð Б à 셤 ठे 셤 à 유 셤 셤 8 ଚ à

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26-MAX-2000; 2000US-02067427P.
23-OCT-2000; 2000US-0245578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
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antibacterial, drug design
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Xu HH;
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P-PSDB; AAU356999.
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Yamamoto RT,
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nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Matches 1307; Conservative
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia soli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonaa earuginosa and Entercoccus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins eantibodies compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous

Claim 27; SEQ ID NO 8195; 511pp; English.

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                                                                                                    CAACCACACATTTCTCTCTAGAACACAGGCATTTTTAAATGAATTTTGCAGAAAGTTTAAGT
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                                      982 AGGCTACAATTGAAACAGCACGAAAAAAATATCCACATAAAGAAGTTGTTGCAGTATTT
                                                                     1042 CAACCACACATTTCTCTCTAGAACACAAGCATTTTTAAATGAATTTGCAGAAAGTTTAAAGT
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13-FEB-2002 (first entry)

Staphylococcus aureus DNA for cellular proliferation protein #77.

Antisense, ds, prokaryotic cellular proliferation gene, antibiotic, antibacterial; drug design.

Staphylococcus aureus. WO200170955-A2

21-MAR-2001; 2001WO-US009180 2000US-0191078P 21-MAR-2000;

23-MAY-2000; 2000US-0206848P. 26-MAY-2000; 2000US-020727P. 23-OCT-2000; 2000US-0242578P. 27-NOV-2000; 2000US-0253625P. 2000US-0257931P 16-FEB-2001; 2001US-6269308P 22-DEC-2000;

(ELIT-) ELITRA PHARM INC

Ohlsen KL, Xu HH; WPI; 2001-611495/70. Haselbeck R, Yamamoto RT,

Carr GJ;

Zyskind JW, Wall D, Trawick JD,

P-PSDB; AAU33801.

οĘ polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids

SEQ ID NO 4242; 511pp; English Claim

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes,

their use in the discovery of novel antibiotics, the essential genes
themselves and the encoded proteins. The prokaryotes used are Escherichia
coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
Pseudomonas aeruginosa and Esterococcus faccalis. The invention is also
useful for the identification of potential new targets for antibiotic
development. The antisense nucleic acids can also be used to identify
proteins used in proliferation, to express these proteins, and to obtain
antibodies capable of binding to the expressed proteins. The proteins can
cantisense nucleic acids sequence is also useful to screen for nomologous
nucleic acids which are required for cell proliferation in a wide variety
of organisms. The present sequence encodes an essential prokaryotic
collular proliferation protein. Note: The sequence data for this patent
did not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
tp. wipo.int/pub/published_pct_sequences ô 240 240 780 120 120 180 180 300 300 360 420 480 540 540 600 099 720 360 420 480 009 99 9 9 1 ATGACACACTATCATTTGTCGCAATDAAGGTTCTCGCCATGAGTTCATTAGCACAAATC 1 ATGACACACIATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC AIGCAIGAITIAGGACAIGAAGIICAAGGAICGGAIATIGAGAACIACGIAITIACAGAA 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 121 GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGGTGCTAATAACATAAAAAA 181 GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA 241 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTATTAAA GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAC 721 ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT GTTGCTCTTAGAATTAAGGGGGTTAAAATATTACCATTTGATGCTAATAACATAAAAGAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATGITATGAATGGTGATAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGG TIGCCIGAAAGIGATIATITCGCTITITGAGGCATGIGAATATAGACGTCACTITITAAGI TIGCCTGAAAGTGATTATTTTGCCTTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTTACGGATAAAGGT Gарв .. 0 4; Length 1311; Sequence 1311 BP; 462 A; 164 C; 250 G; 435 T; 0 U; 0 Other; 7; Indels Score 954; DB Pred. No. 0; 0; Mismatches Query Match 72.4%; Best Local Similarity 99.5%; Matches 1304; Conservative 61 121 181 241 301 361 361 421 421 481 481 541 541 601 601 661 661 8 셤 à 셤 ଚ 원 a à 요 qq 8 셤 à g ð 셤 à 쉽 8 셤 à 셤 à à ઠ

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ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT 780
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/gene= "MurC"
/product= "UDP-N-acetylmuramate:L-alamine ligase (MurC
polypeptide)"
                                                                                                                                                                                                                                                                                                                                                                                    GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAAGCTA
                                                                        GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT
                                                                                              GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT
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                                                                                                                                                                                                                       CAACCACACATTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAAGT
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                                                                                                                                                                                                                                                                                                                      UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoding DNA.
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bacterial;
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The present sequence represents a MurC gene encoding a Staphylococcus aureus UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide). Host cell contraining an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially S. aureus) infections. They are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising attibodies, to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The MurC gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant MurC gene; increment in antisense/ribozyme therapeutics; to detect mutant MurC gene; increments in the contrained in antisense in the 
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                                                                                                                 Murc polypeptide from Staphylococcus aureus and related - useful in diagnosis, treatment and prevention of bacterial
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                                                                                                                                                                                                                 Claim 2; Page 3-4; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.9%;
Best Local Similarity 99.6%;
Matches 1042; Conservative
  Burnham MKR
                                               1999-062655/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                   New isolated Murc
nucleic acid - use
                                                                      P-PSDB; AAW87771
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  Wallis NG,
                                                                                                                                                                      infections.
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can lake be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used the meaning are useful as primers or probes for isolating headable meading.
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                             Polynucleotide(s) and proteins derived from Staphylococcus aureus -
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                                                                                              Claim 1; Page 1287-1288; 3271pp; English.
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Rosen CA;

Fannon MR,

Dillon PJ,

Barash SC,

Choi GH,

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Kunsch

96US-0009861P

05-JAN-1996; 07-JAN-1997;

97EP-0010011

EP786519-A2. 30-JUL-1997 (HUMA-) HUMAN GENOME SCI INC

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240 965

The invention relates to a UDD-N-acetylmuramate:L-alanine ligase (Murc polypeptide) encoded by the S. aureus Murc gene. Host cells containing an expression system comprising the Murc gene can be used for the ceppression system comparising the Murc gene can be used for the comparising the polypeptide. Againsts or the Murc polypeptide are used to treat conditions requiring increased activity or competitive polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide acid or competitive polypeptide are useful for infections. They are also useful against the antibacterial agains and related cancers, ulcers and gastritis. The antibacterial agains are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The Murc polypeptide is also useful for of bacteria to matrix proteins. The Murc polypeptide is also useful for antibodies; to identify modulators or specific receptors; in rational custing dealing and as an immunogen for vaccines. The Murc gene sequences are to chromosomal mapping; to determine bacterial serotype; and for genetic 1801 GIGCATCGITAAITAAIGAAGATICTATIAAIGAIGTATAGAACAAITIGAIAAIGCIGITA 1860 1861 TITIATITATGGGGGGGGGATATTCAAAATTACAAAATGCATATTTAGATAAATTAG 1920 New isolated MurC polypeptide from Staphylococcus aureus and related nucleic acid - useful in diagnosis, treatment and prevention of bacterial GTGCATCGTTAATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTA TTTTATTTATGGGTGCAGGTGATATTCAAAAATTACAAAATGCATATTTAGATAAATTAG Murc gene; UDP-N-acetylmuramate:L-alanine ligase; Murc polypeptide; bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine; immunogen; drug; genetic immunisation; ds. /*tag= a /product= "partial MurC polypeptide" Partial nucleotide sequence of the Murc gene. Location/Qualifiers GCATGAAAATGCGTTTTAA 1314 1921 GCATGAAAATGCGTTTTAA 1940 Claim 2; Page 4-5; 39pp; English. (SMIK) SMITHKLINE BEECHAM CORP. (SMIK) SMITHKLINE BEECHAM PLC. AAV80065 standard; DNA; 660 BP 98EP-00305064. 97US-0052720P. (first entry) .660 Burnham MKR; Staphylococcus aureus. WPI; 1999-062655/06. P-PSDB; AAW89199 26-JUN-1998; 17-MAR-1999 03-JUL-1997; EP889123-A2 07-JAN-1999 Wallis NG, infections. 1175 1235 1295 AAV80065; ਨੇ g 8 셤 à g

TACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTTCAACC 1025 120 905 Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; antibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic; TITICAIGIGIAGIGCAIGCIGACIITIAIGAICACIICCICICICCACAAIAIGCIGA 121 CCATACAGTITIAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTAGATGT 666 ATTIAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGTACTGC 1 ATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAGGTACTGC 846 TACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTACAATGAAAC 181 TACAAATATTAAAGAAGCATTAGAAACGTTTAGATGATAAACGTCGTTTCAATGAAAC 906 TACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAAAATTAGTGC CCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTAGATGT Gaps immunisation. The present sequence represents a partial nucleotide sequence (Murc ORF) of the Murc gene DNA encoding a Staphylococcus aureus protein of unknown function. Reichard RW, Nicholas RO; Ward JM, Lonetto MA; ö 25.0%; Score 330; DB 2; Length 660; 99.7%; Pred. No. 2.3e-142; ive 0; Mismatches 1; Indels Sequence 660 BP; 233 A; 83 C; 120 G; 224 T; 0 U; Knowles DJC, Rosenberg M, 1026 ACACACTTTCTCTAGAACACA 1046 (SMIK) SMITHKLINE BEECHAM CORP. (SMIK) SMITHKLINE BEECHAM PLC. BP. 97EP-00307485. 96US-0027032P. AAV53479 standard; DNA; 619 30-OCT-1998 (first entry) fatches 380; Conservative Hodgson JE, l, Pratt JM, Staphylococcus aureus. Best Local Similarity WPI; 1998-252940/23. P-PSDB; AAW77686. Black MT, Ho Burnham MKR, 24-SEP-1997; 24-SEP-1996; therapy; ss. 13-MAY-1998 EP841394-A2 726 996 Query Match 984 241 301 AAV53479; RESULT 11 AAV53479/c ន្តដូនូ 셤 ద à Š ઠે 셤 δ a ò a à 요 ď 셤

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function, and represents a DRA Sequence of the invention. The DNA sequences were isolated from Staphylococcus aureus WGHU29 (NCIMB 40711). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, particulated, central nervous, eye, kidney, uninary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection
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                      - useful in
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                  nucleic acid sequences from Staphylococcus aureus WCHU29 - useful ines and for treatment of bacterial infections of e.g. respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 619;
                                                                                                                                                                                                                                                                                                                                                                               Sequence 619 BP; 208 A; 117 C; 79 G; 215 T; 0 U; 0 Other;
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Best Local Similarity 99.7%; Pred. No. 6.3e-117;
Matches 325; Conservative 0; Mismatches 1;
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                                                                                     Claim 1; Page 146; 390pp; English.
                                   vaccines and for treatment of bac
tract and central nervous system.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes to their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus arengoneal are Escherichia coli, Staphylococcus and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic cavidates apple of binding to the expresse these proteins, and to obtain the proteins used in proliferation, to expresse these proteins, and to obtain the bensed to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense oligonucleotide of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly the man will be the printed specification, but was obtained in electronic format directly the printed specification, but was obtained in electronic format directly are the printed specification.
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                                                                                                                                                                                         Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 TGATTTTTTAGGACAGATTATTGATCAATATACTTCAGTAGCTGTAACTGGTGCACATGG
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                                                                                                                                                                                         Trawick JD,
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                                                                                                                                                                                                                                                                                   polynucleotides for the identification and development
                                                                                                                                                                                                                                                                                                       antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 257 BP; 84 A; 50 C; 31 G; 92 T; 0 U; 0 Other;
                                                                                                                                                                                       Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 2928; 511pp; English.
                                                                                                                                                                                         Zyskind JW
             23-MAY-2000; 2000US-0226648P.
26-MAY-2000; 2000US-020648P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-025362F.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
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(first entry)
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Best Local Similarity 100.
                                                                                                                                                                                       Ohlsen KL,
Xu HH;
                                                                                                                                                  (ELIŢ-) ELITRA PHARM INC
                                                                                                                                                                                                                                              WPI; 2001-611495/70.
                                                                                                                                                                                     Haselbeck R,
Yamamoto RT,
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ACA17633
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
contisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide or its fragment whose expression is inhibited by the
cut isolypeptide or its fragment whose expression is inhibited procut proliferation or the activity of a gene in an operon required for
proliferation or the activity of a gainst a biological pathway
control for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation of an
compound's activity; (1) a culture comprising strains in which the proliferation-required gene or its gene
compound's activity; (1) a culture comprising strains in which the screen
compound's activity; (1) a culture comprising strains in which the
compound's activity; (1) a culture comprising strains in which the
compound's activity; (1) a culture comprising strains in which the
compound's activity; (1) a continue compound that inhibits the
compound's activity; (1) a continue compound that inhibits in the
compound's activity; (1) a continue compound that inhibits or conflection of
cutarians, or (13) identifying the target of a compound that inhibits the
compound's province or content or conflection of
cutarian and province or conflection of an ordanian and province and ordanian are not or ordinal for
compound the province or ordinal province or ordi New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, Antisense; 88; prokaryotic essential gene; cell proliferation; Prokaryotic essential gene antisense oligonucleotide #5503. Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Claim 1; SEQ ID NO 5503; 1766pp; English. Malone C, Carr GJ, 06-SEP-2001; 2001US-00948993. 25-007-2001; 2001US-0342923P. 08-FEB-2002; 2002US-0072851. 06-MAR-2002; 2002US-032851. 21-MAR-2002; 2002WO-US009107. 2001US-00815242, (ELIT-) ELITRA PHARM INC Prewick JD, WPI; 2003-029926/02, Zamudio C WO200277183-A2 21-MAR-2001; drug design: 33-OCT-2002 Archaea. Wang L,

Zyskind JW; Xu HH;

Sequence 257 BP; 84 A; 50 C; 31 G; 92 T; 0 U; 0 Other;

ö Gapa ÷0 19.5%; Score 257; DB 7; Length 257; 100.0%; Pred. No. 1.4e-108; trive 0; Mismatches 0; Indels Matches 257; Conservative Local Similarity Query Match

332 GAGTAGCCATGAAGAATAGTACGTGCACATCAATTGAAATTAGATGTTGTAAGTTATAA 138 TAAAACTICTACAACAGGTITAATTATCACATGTTATGAATGGTGATAAAAAGACTTCATT 392 TAAAACTICTACAACAGGTTTATTATCACATGTTATGAATGGTGATAAAAAGACTTCATT 18 rearrititaggacagarratrgarcaararacricagraecrgraacrigerecared 78 Staphylococcus aureus cellular proliferation inhibitory sequence #246. TGATTTTTTAGGACAGATTATTGATCAATATACTTCAGTAGCTGTAACTGGTGCACATGG GAGTAGCCATGAAGAAATAGTACGTGCACATCAATTGAAATTAGATGTTGTAAGTTATAA Carr GJ; Antisense; ss; prokaryotic cellular proliferation; antibiotic, AAS49022 standard; DNA; 225 BP. TTTAATTGGTGATGGCA 409 2000US-0206849P. 2000US-0207727P. 2000US-0242578P. 2000US-0253625P. 2000US-0257931P. 21-MAR-2001; 2001WO-US009180. rrraarregrearesca 1 2000US-0191078P. drug design 13-FEB-2002 (first entry) (BLIT-) ELITRA PHARM INC Staphylococcus aureus. antibacterial; WO200170955-A2 21-MAR-2000; 23-MAY-2000; 23-OCT-2000; 27-NOV-2000; 22-DEC-2000; 16-FEB-2001; 26-MAY-2000; 27-SEP-2001 257 213 197 273 137 333 77 393 17 AAS49022; RESULT 14 AAS49022, g 셤 ઠે 셤 셤 ò 셤 Š Š

Trawick JD, Zyskind JW, Wall D, Haselbeck R, Ohlsen KL Yamamoto RT, Xu HH;

WPI; 2001 611495/70

ö New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.

Claim 1; SEQ ID NO 1599; 511pp; English.

the 6213

patent did not form part of the printed specification, but was obtained K. pneumoniae or P. aeruginosa. The present sequence is one of the 621: antisense sequences of the invention. Note: The sequence data for this

in electronic format directly from WIPO at the out of the contract of the cont

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Miebsiella pneumoniae, Pseudomonas aeruginosa and Enerococcus faecalls. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous

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nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense oligonuclectide of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                          Score 225; DB 4; Length 225; Pred. No. 8.8e-94;
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16-FEB-2001; 2001US-0269308P.
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27-NOV-2000;
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themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonalla typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense oligonucleotide of the invention. Note: The sequence data for this patent did not form part of from WIPO at ftp.wipo.int/pub/published_pot_sequences
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-712-713-1 1318

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IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

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6747726 hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0
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Maximum Match 100%
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Database

N_Geneseq_29Jan04:* 1: geneseqn19808:* geneseqn2001as:* geneseqn2001bs:* geneseqn2003ag:* geneseqn1980s:* geneseqn1990s:* geneseqn2002s:* geneseqn2000s:*

geneseqn2003bs:* geneseqn2003cs:* geneseqn2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aas00189 S. aureus	Add15462 Staphyloc	Add15464 Staphyloc	Acf72770 Staphyloc	Aca19726 Prokaryot	Aas54558 Staphyloc	Aas51660 Staphyloc	Aav99650 UDP-N-ace	Aav74703 Staphyloc		Aca47124 Prokaryot	Aav80065 Partial n	Aca22277 Prokaryot	Aav53479 DNA encod	Aas53136 Enterococ	Aca33252 Prokaryot	Continuation (17 o	Abg67195 Listeria	Continuation (2 of	Aca36934 Prokaryot	Continuation (17 o	Aca33597 Prokaryot	Aca47261 Prokaryot
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ALIGNMENTS

AAS00189 standard; DNA; 1318 BP.

AAS00189;

(first entry) 04-JUL-2001 S. aureus DNA encoding UDP-N-acetylmuramate:L-alanine ligase, MurC.

UDP-N-acetylmuramate:L-alanine ligase; MurC; immunogen; vaccine; antibody; wound infection; cellulitis; burn infection; eyelid infection; food poisoning; joint infection; neonatal conjunctivitis; osteomyelitis; skin infection; scalded skin syndrome; toxic epidermal necrosis; Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis;

Staphylococcus aureus.

Location/Qualifiers 1. .1314 /*tag= a /product= "MurC" Key

WO200116292-A2

08-MAR-2001.

31-AUG-2000; 2000WO-US023773. 99US-0151933P. 01-SEP-1999;

(HUMA-) HUMAN GENOME SCI INC.

Choi GH;

WPI; 2001-183259/18. P-PSDB; AAU00828 New isolated nucleic acid for use in diagnosing Staphylococcus infections and in vaccines for eliciting immune responses to the infections.

Claim 1; Page 14; 225pp; English.

The sequence encodes S. aureus MurC (UDP-N-acetylmuramate:L-alanine ligase). The polynucleotides of the invention are used to detect

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1080 1080 1200

1318

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ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTATTGGGTGCAGGTGATATT 1260
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; 2001US-0334692P.
; 2001US-033934P.
; 2001US-0350973P.
; 2001US-033866P.
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29-OCT-2001;
30-OCT-2001;
27-NOV-2001;
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25-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus nucleic acids in a biological sample from an animal for diagnosing Staphylococcus infections. The polypeptides of the invention are used to detect anti-Staphylococcus infections. The polypeptides from an animal to diagnose Staphylococcus infections. The polypeptides are also used in vaccines to elicit protective antibodies in an animal to a member of the Staphylococcus genus and for preventing or attenuating an infection caused by a member of the Staphylococcus genus e.g wound infection caused by a member of the Staphylococcus genus e.g wound infection, cellulitis, burn infection, eyelid infection, food poisoning, coint infection, neonatal conjunctivitis, osteomyelitis, skin infection, scalded skin syndrome (also known as toxic epidermal necrosis, Ritter's disease and Lyell's disease), toxic shock syndrome and endocarditis. The polymoclocides may also be used in vaccines and for preventing or attenuating a Staphylococcus infection. Antibodies to the polypeptides may be used to purify, detect and target the polypeptides in in vitro and therapeutic methods
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100.0%; Pred. No. 2.7e-249;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 1318; Conservative
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Vedadi M, Alam MZ, Awrey D, Beattie B; Kanagarajah D, Nethery K, Ng I, Mansoury K; Viola C, Wrezel O;

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Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria.
                                                                                                                                         Claim 20; SEQ ID NO 27; 325pp; English.
18-DEC-2001; 2001US-0341732P.
18-DEC-2001; 2001US-0341776P.
19-DEC-2001; 2001US-0341949P.
                                (AFFI-) AFFINIUM PHARM INC
                                                Dharamsi A,
Houston S,
Pinder B,
                                                                                WPI; 2003-468119/44.
P-PSDB; ADD15463.
                                                Edwards A,
Domagala M,
Mcdonald M,
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This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus), Streptococcus preumoniae (S. pneumoniae) and Sacherichia coli (E. coli) that provide novel antimicrobial targets. Specifically, it refers to critical role in the life cycle and viability of their pathogenic species of critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate characterisation by labelling with isotopic or heavy atoms, and also fusion proteins. These proteins provide structural and functional information to aid the discovery of therapeutic molecules to treat disorders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as a natigen for vaccination purposes. The polypeptides are also useful for develophing antimicrobial agents for use as surface disinfectants, personal hygiene applications and as food preservatives or in treating for sequence is DNA predicted from the genomic sequence of S. aureus UDP-Nacetylmuramate-alanine ligase (murC) of the invention.

Sequence 1335 BP; 472 A; 161 C; 255 G; 447 T; 0 U; 0 Other;

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180 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 120 AIGCAIGAITIAGGACAIGAAGITCAAGGAICGGAIATITGAGAACTACGIAITIACAGAA 141 201 240 261 300 321 360 INTERCRITAGE TO THE FORM OF THE TRANSPORT OF THE TRANSPOR 420 9 GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAGAA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA 1 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAGAA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA CATGTTATGAATGGTGATAAAAAGACTTCATTTTAATTGGTGATGGCACAGGTATGGGA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA Gaps ö Length 1335; Query Match

99.7%; Score 1314; DB 9; Length 1.
Best Local Similarity 100.0%; Pred. No. 1.6e-248;
Matches 1314; Conservative 0; Mismatches 0; Indels 121 142 181 202 241 262 301 322 361

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हे ह	721 ACTGC	TITIGATGIGIATALGIGGARGGIGAGITITIA IGATCACTITCCIGICTCCACAATAT .	780
g ;	742 ACTGC	TTTTGATGTATGTAGGATGGTGTTTTATGATCACTTCCTGTCTCCACAATAT	801
ž 8	/81 GGTGA(81 GGIGACCHACAGITIIAANIGCATIAGCIGTAATIGCGATTAGTTATTTAGAGAAGCTA 840 	840 861
8 8	841 GATGT	TACAAATATTAAAGAAGATTAGAAACGTTTGGTGGTGGTGAAACGTCGTTTCAAT S	900
8 6	862 GATGT	TACAAATATTAAAGAAGCATTAGAAACGTTTTGGTGGTGTTAAAGGTCGTTTCAAT	921
B 5	901 GAAAC 922 GAAAC	GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT 9 	960
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ф	1102 AAAGC		1163
ð :	4	TTAACGATACAAGATTTAATTGATAAAATTGAAGGTGCATCGTTAATTAA	20
g	27		1221
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à	1261 CAAAAA	TTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314	
qq	 1282 CAAAAA		
RESULT 3 ADD15464 ID ADI	15464	rd; DNA; 1335 BP.	
X Z	ADD15464;		
4	15-JAN-2004 (first entry)	irst entry)	
E S	Staphylococcus	aureus murc DNA (SeqID 29).	
22	microbial; anti-	microbial; antimicrobial; membrane biosynthesis; pathogenic; immunological response; vaccination; surface disinfectant;	
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Beattie B; I, Mansoury K;

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personal hygiene application; food preservative; ds; gene; UDP-N-acetylmuramate-alanine ligase.
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Kanagarajah D, Nethery K,
Viola C, Wrezel O;
                                                1. .1335
/*tag= a
/product= "MurC protein"
                                                                                                                                                                                                                                                                                                      20; SEQ ID NO 29; 325pp; English.
                                     Location/Qualifiers
                                                                                                                   21-SEP-2001; 2001US-0323992P.
21-SEP-2001; 2001US-0324152P.
25-SEP-2001; 2001US-0339924P.
29-OCT-2001; 2001US-0339924P.
30-OCT-2001; 2001US-0339924P.
31-NOV-2001; 2001US-033966P.
31-NOV-2001; 2001US-0331666P.
31-NOV-2001; 2001US-0341732P.
31-DEC-2001; 2001US-0341776P.
                                                                                                      20-SEP-2002; 2002WO-CA001428
                                                                                                                                                                                                      (AFFI-) AFFINIUM PHARM INC.
                                                                                                                                                                                                                    Dharamsi A,
Houston S,
Pinder B,
                       Staphylococcus aureus
                                                                                                                                                                                                                                                   2003-468119/44.
                                                                                                                                                                                                                                                        P-PSDB; ADD15465
                                                                          WO2003025007-A2
                                                                                                                                                                                                                    Edwards A,
Domagala M,
Mcdonald M,
                                                                                                                                                                                                                                                                                                       Claim
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This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus), Streptococcus preumoniae (S. pneumoniae) and Sacherichia coli (B. coli) that provide novel antimicrobial targets 'Specifically, it refers to polypeptides that are involved in membrane biosynthesis, which play a critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate invention describes modified version of these proteins that facilitate information to aid the discovery of therapoutic molecules to treat disorders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for developing antimicrobial agents for use as surface disinfectants, an antigen for vaccination purposes. The polypeptides are also useful for personal hygiene applications and as food preservatives or in treating food products to eliminate potential pathogens. This polynucleotide sequence is the experimentally pradicted DNA of S. aureus UDP-N-Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria.

Sequence 1335 BP; 472 A; 160 C; 255 G; 448 T; 0 U; 0 Other; Query Match
Best Local Similarity 99.9%;
Matches 1313; Conservative

81 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC

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Indels

Score 1312.4; DB 9; Pred. No. 3.4e-248; 0; Mismatches 1;

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Length 1335;

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61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 120

1102 AAAGCAGATTCTTATTTTTTTTTTTTTTTTTTTAATTATAGAAAATTACTGCGCA 1161 300 360 420 480 540 999 441 501 561 600 621 681 720 741 780 840 900 960 321 861 981 801 921 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA TATACTICAGIAGCIGIAACIGGIGCACAIGGIAAAACIICIACAACAGGITITAILAA TTGCCTGAAAGTGATTATTTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT TATAAACCTGATTACGCAATTATGACAAAATATTGATTTCGATCATCCTGATTATTAAA ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTAGGACAGATTATTGATCAA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTTAGGACAGATTATTGATCAA cangitalicaarcaraaaagacitcaritiraarregigaregcacacacaraega TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA ATTGCTTGGGGTGATGAAGATTACGTAAAATTGAAGCAGATGTTATTATTAT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT 982 AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT GTTGCTCTTAGAAATAAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA CATGITATGAATGGTGATAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGG TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAAGGTATT 601 ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTAFTAT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT 742 ACTGCTTTTGATGTGTTGTGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGGAAGCTA GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT 922 GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCCATCCAAGAGAATT GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT 1042 CAACCACACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT CAACCACACACTITICTCTAGAACACAGGCATTITITAAATGAATTITGCAGAAAGTITAAGT <u>AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA</u> AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTT 322 142 202 262 382 442 481 502 295 622 721 82 121 181 241 541 1141 301 361 421 661 682 781 802 841 862 961 1021

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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused S. aureus, e.g. sepsis.
                                   CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the novel S. aureus genes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID NO 899; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  Scarselli
                                                                                                                                             Bb.
                                                                                                                                                                                                          Staphylococcus aureus DNA #450
                                                                                                                                           DNA; 1332
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                                                                                                                                                                                    (first entry)
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Matches 1311, Conservative
                                                                                                                                                                                                                                                                Staphylococcus aureus
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
                                                                                                                                             essential gene; cell proliferation;
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                                 1282 CAAAATTACAAATGCATATTTAGATAAATTAGGCATGAAAATGCGTTT
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Forsyth RA,
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Yamamoto R,
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                                                                                                                           Prokaryotic essential gene #1383
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                                                                           ACA19726 standard; DNA; 1314
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0072251.
06-WAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                     2'1-MAR-2002; 2002WO-US009107
                                                                                                                                     ds; prokaryotic e
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                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                     Staphylococcus aureus
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Trawick JD,
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                                                                                                                                                    drug design;
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or nucleic acid; (3) a most cell containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the artisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of agene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, (6) identifying a gene required for cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound, sactivity; (11) a culture comprising strains in which the gene or which he set or compound the activity is overspressed or underexpressed; (12) determining the extent or which he are in a companiant. to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids The invention relates to an isolated nucleic acid comprising any one

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required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                        Length 1314;
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                                                                                                         Sequence 1314 BP; 464 A; 161 C; 250 G; 439 T; 0 U; 0 Other;
                                                                                                                                     Score 1310.8; DB 7; Length
Pred. No. 7e-248;
0; Mismatches 2; Indels
                                                                                                                                      99.54;
                                                                                                                                                  Best Local Similarity 99.8
Matches 1312; Conservative
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721 ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACACATAT
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Pred. No. 2.6e-246;
0; Mismatches 7;
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Best Local Similarity 99.5%;
Matches 1307; Conservative
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GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT
            1021 CAACCACACTITICITIAGAACACAAGCAITITIAAAIGAAITIGCAGAAAGITIAAGI
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                                                                                                                                                                                                                                                                                                                                                                               cellurar proliferation gene; antibiotic;
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2000US-0207727P.
2000US-0242578P.
2000US-0253625P.
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                                                                                                                                                                                                                                                                                                    standard; DNA; 1335
                                                                                                                                                                                                                                                                                                                                                                                Antisense, ds; prokaryotic antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                          (first entry)
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Yamamoto RT, Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus
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26-MAY-2000;
23-OCT-2000;
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16-FEB-2001;
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their use in the discovery of novel antibiotics, the essential genes
themselves and the encoded proteins. The prokaryotes used are Escherichia
oil, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
Pseudomonas aeruginosa and Enterococcus facealis. The invention is also
useful for the identification of potential new targets for antibiotic
development. The antisense mucleic acids can also be used to identify
proteins used in proliferation, to express these proteins, and to obtain
antibodies capable of binding to the expressed proteins. The proteins can
entisense nucleic acids sequence is also useful to screen for homologous
nucleic acids which are required for cell proliferation in a wide variety
of organisms. The present sequence encodes an essential prokaryotic
collular proliferation protein. Note: The sequence data for this patent
did not form part of the printed appecification, but was obtained in
electronic format directly from WIPO at

ttp.wipo.int/pub/published_pct_sequences 120 180 240 300 360 480 540 900 099 720 780 141 261 420 621 741 201 321 381 441 501 561 681 9 81 ATGCATCATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTTAGGACAGATTATTGATCAA 322 TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATA 22 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 142 GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGGTGCTAATAACATAAAAGAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT 562 GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT 601 ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT 622 ATTGCTTGGGGTGATGATGACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAC 661 TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT 682 TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTATACGATAAAGGT TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTTAAGT 481 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCGTGATTATTTTTAAA 1 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATGITATGAATGGTGATAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA 442 TIGCCIGAAAGIGATIATITICGCITITIGAGGCAIGIGAATATAGACGICACTITITAAGI Gaps 4; Length 1335; ö Sequence 1335 BP; 472 A; 164 C; 255 G; 444 T; 0 U; 0 Other; Indels

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ACTGCTTTTGATGTGTATGTGGTGATGTTTTATGATCACTTCCTGTCTCCACAATAT
                                                                      GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTTAAAACGTCGTTTCAAT
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Xu HH;
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26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-025362F.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
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Yamamoto RT,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Seudomonas aeruginosa and Enterococcus faccalls. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The proteins can be used to screen compounds in rational drug discovery programmes. The nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in clectronic format directly from WIPO at the wipo int/pub/published_pct_sequences
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                                                  New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoding DNA
                                                                              MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;
bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine;
immunogen; drug; genetic immunisation; ds.
                                                                                                                                               Location/Qualifiers
AAV99650 standard; DNA; 1351 BP
                                          (first entry)
                                                                                                                                                          .1335
                                                                                                                            Staphylococcus aureus.
                                         17-MAR-1999
                     AAV99650
                                                                                                                                                Key
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The present sequence represents a MurC gene encoding a Staphylococcus aureus UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide). Host cell containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (sepecially S. aureus) infections. They are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising aruthodies; to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The MurC gene sequences are useful in antisense/riboxyme therapeutics; to detect mutant MurC gene; for chromosomal mapping; to determine bacterial serotype; and for genetic
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                                                                                                                                                                                                                                                                                                      New isolated MurC polypeptide from Staphylococcus aureus and related nucleic acid - useful in diagnosis, treatment and prevention of bacterial
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                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 3-4; 39pp; English
                                                                                                                                       SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.
                                                                                               97US-0052720P.
                                                      98EP-00305064.
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                                                                                                                                                                                                                                               WPI; 1999-062655/06.
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/*tag= a /gene= "MurC" /product= "MDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide)"

EP889123-A2

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cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

/*tag= a /note= "these bases represent a line of missing text in /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

Location/Qualifiers 1141. .1200

misc_feature

Staphylococcus aureus

Rosen CA;

Dillon PJ, Fannon MR,

Barash SC,

Choi GH,

Kunsch CA,

WPI; 1997-374922/35

(HUMA-) HUMAN GENOME

97EP-00100117. 96US-0009861P.

07-JAN-1997; 05-JAN-1996;

EP786519-A2 30-JUL-1997 rolynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of a S.aureus vaccines.

Claim 1; Page 1287-1288; 3271pp; English.

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The colypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock of for recombinant production of the polypeptides. The new DNA sequences can be used to the including cellulities are useful as primers or probes for isolating computer and their fragments) are useful as primers or probes for isolating to a computer and the computer are alsolating contained on the computer and the computer and the computer are contained on the computer and the computer 
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08-NOV-1997;
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
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the inventor relates to an interest and compilating any order the following any transfer the following any transfer the following any transfer the following a product operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding attisense mucleic acid; (4) an antibody capable of specifically binding colliferation or the activity of agence in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits proliferation of the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling a product is overexpressed or underexpressed; (12) determining the extent or owhich each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. preumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at screening Zyskind JW; Xu HH; S New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs. ds; prokaryotic essential gene; cell proliferation; invention relates to an isolated nucleic acid comprising Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Claim 14; SEQ ID NO 34994; 1766pp; English. ftp.wipo.int/pub/published_pct_sequences Prokaryotic essential gene #28781 Malone C, Carr GJ, 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P 21-MAR-2002; 2002WO-US009107 Staphylococcus epidermidis (first entry) (ELIT-) ELITRA PHARM INC. Zamudio C, Trawick JD, WPI; 2003-029926/02. P-PSDB; ABU43254. WO200277183-A2 19-JUN-2003 03-OCT-2002. Antisense; ηď Wang Wall drug

1311 BP; 473 A; 181 C; 243 G; 414 T; 0 U; 0 Other; Sequence

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The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoded by the S. aureus MurC gene. Host cells containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists nor the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially S. aureus) infections. They are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MurC polypeptide from Staphylococcus aureus and related - useful in diagnosis, treatment and prevention of bacterial
                                                                           1081 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
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                                                                       TTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC
                                  ;
   Length 1311;
                                    Indels
 Score 915.8; DB 7;
Pred. No. 2.2e-170;
); Mismatches 247;
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69.5%;
ilarity 81.2%;
Conservative
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Best Local Simil
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                  of bacteria to matrix proteins. The Murc polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify wodulators or specific receptors; in rational drug design and as an immunogen for vaccines. The Murc gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant Murc gene; immunisation. The present sequence represents a partial nucleotide sequence (Murc ORF) of the Murc gene
  infection prevention or generally as wound treatments to prevent adhesion
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                                                                                                                                                                                                                                                                     48.0%; Score 633; DB 2; Length 660; 98.5%; Pred. No. 6.1e-115; ive 0; Mismatches 10; Indels
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                                                                                                                                                                                                                             Sequence 660 BP; 233 A; 83 C; 120 G; 224 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                    639; Conservative
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The invention relates to an isolated nucleic acid compilating a promoter of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid enodding a promoter operably linked to the nucleic acid enodding a promoter operably linked to the nucleic acid comprising a promoter operably linked by the antisense and polypeptide whose expression is inhibited by the antisense outleic acid; (2) a host cell containing the vector; (3) an isolated of antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation of the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiocit; (10) profilling a compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for estrains; or (13) identifying the target of a compound that inhibits the control of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, contradicate dor proliferation in cells other than S. aureus, S. typhimurium, contradicate dor proliferation in cells other than S. aureus, S. typhimurium, contradicate of the printed specification, but was obtained in all and the present sequence dor this patent did contradication of the present sequence are one of the target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 120
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                                                                                                                                                                                                                                                                                                                                                                        Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid comprising any
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Forsyth RA,
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Matches 858; Conservative
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Trawick JD,
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                    Bacillus anthracis.
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                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; centiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
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vaccines and for treatment of bacterial infections of e.g. respiratory
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Rosenberg M,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia chambelves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas acruginosa and Enterococcus faccalias. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain attibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The autisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent cit form part of the printed specification, but was obtained in electronic format directly from WIDO at electron
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                                                                                            New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1371 BP; 436 A; 236 C; 296 G; 403 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 555; DB 4; Length 13
Pred. No. 1.4e-99;
0; Mismatches 455; Indels
                                                                                                                                                         Claim 27; SEQ ID NO 6773; 511pp; English.
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Best Local Similarity 64.7%;
Matches 841; Conservative
                                2001-611495/70
                                                      P-PSDB; AAU35277
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AATATGGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTAGAGA
                                                                                                                                                                             TAAGTAAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTG
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                                                               AATATGGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGA
                                                                                                                                                   AGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTT
                                                                                                                                                                                                                                      TCAATGAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAG
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26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
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Xu HH;
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G|CAGTGACATGATTATTGATGATTATGCGCACCATCCAGCTGAAATTAAAGCAACG 1017
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                                                                                                                                                                                                                                                   910 AITGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATTAGTGCTACA 969
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                                               670 AAAGATTCGGATGACATTTATGCTCAAAATATTTCAAATTACGGATAAAGGTACTGCTTTT
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Search completed: June 6, 2004, 00:10:04 Job time : 642 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

June Run on:

5, 2004, 23:46:19; Search time 134 Seconds (without alignments) 5458.398 Million cell updates/sec

US-10-712-713-1 1318 1 atgacacactatcattttgt.....gaaaaatgcgttttaagctt 1318 Title: Perfect score: Sequence:

Scoring table:

682709 seqs, 277475446 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched:

1365418

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB 6

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:*
1: /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Segmence 392. App	2296	Semience 179. Ann			16	16	Sequence 61. Appl	61.	61	61,	115.	115	3260.		89	_	27	ø	H	7	۳.	Ή.	9	Ι.	ì	1,
SUMMAKIES	ID		US-08-956-171E-392	US-09-134-001C-2296	US-08-936-165A-179	-08-961-527-61	38-940-572	-08-714-918	-315	39-265-315	US-09-266-417-61	US-09-528-709-61	-745	US-08-961-083-115	US-09-536-784-115	US-09-107-532A-3260	m	US-09-328-352-897	US-09-790-988-1	US-09-543-681A-2779	US-09-557-884-1	US-09-643-990A-1	US-09-198-452A-1	US-08-973-462-2	US-08-973-462-1	US-09-543-681A-601	US-08-446-855A-1	US-09-150-741-1	US-09-557-884-1
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de	Query Match		73.	70.0	43.3	30.4	30.3	29.6	29.6	29.6	29.6	29.6	29.6	28.1	28.1	26.9	23.6	10.5		6.4		•		5.5	5.5	4.5	4.2	4.2	4.1
	Score		1314	922	570.4	400.8	399.2	389.6	89.	389.6	٠	389.6	389.6	370.2	370.2	354.4	310.4	138.6	105.4	84.4	78.4	78.4	76.2	72.8	72.8	58.8	55.2	55.2	54.4
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Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 192, Appl Sequence 11, Appl Sequence 56, Appl Sequence 147, Ap Sequence 11, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7, Appli Sequence 34, Appli Sequence 34, Appli Sequence 63, Appli Sequence 63, Appli Sequence 64, Appli Sequence 64, Appli Sequence 65, Appli	aureus Polymucleotides and Sequences es, Inc. ch, 1.4Mb storage n 6.2 171E	
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Staphylococcus epidermidis
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Best Local Similarity 81.4%;
Matches 1069; Conservative
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    Length 2424;
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 99.7%; Score 1314; DB 4; L
100.0%; Pred. No. 6.4e-296;
iive 0; Mismatches 0;
Query Match
Best Local Similarity 100.
Matches 1314; Conservative
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                                                                                                                                                                                                                                                                                                                                              Sequence 2256, Application US/09134001C
Fatent No. 6380370
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILICA DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PELING DATE: 1997-11-08
PRIOR PELING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
SEQ ID NOS: 5674
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Pred. No. 5.1e-205;
0; Mismatches 245;
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APPLICANT: Pratt, Julie
APPLICANT: Reichard, Richard
APPLICANT: Reschberg, Martin
APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Judith
ITILB OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
ITILB OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS: S34
CORRESPONDENCE ADDRESS:
ADDRESSEE: SMITHKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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98.0%; Pred. No. 1.6e-123;
live 0; Mismatches 11;
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COMPUTER: IBM Compatible
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, CAMPAT R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: PS0549
TRELECOMMULICATION:
MEDICOMMULICATION:
MEDI
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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US-08-936-165A-179
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Best Local Similarity 98.03
Matches 588; Conservative
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TELEX:
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STRANDEDNESS: single
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Patent No. 6348582
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Lonetto, Michael
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
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8 8 8 8 8 8	8 8 8 8 8 8		8 6 8 6 8 6 8	8 8 8 8 8 8 8
Db 256 TATGTAAAGCAGATCGTGTATTGTGGAAATTTTGGCTCAATTAGAGAAAATCTG 197	RESULT 4 US-08-961-527-61/c Sequence 61, Application US/08961527 Sequence 61, Application US/08961527 SENERAL INFORMATION: APPLICANT: Charles Kunsch TITLE OF INVENTION: Streptococcus pneumoniae Polymucleotides and Sequences NUMBER OF SEQUENCES: 391 CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc. STREET: 9410 KeV West Avenue CITY: Rockvilley	STATE: Maryland COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM: MEDIUM TYPES Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 SPETATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text APPLICATION NUMBER: US/08/961,527 FILLING DATE: FILLING DATA: PRIOR APPLICATION DATA:	FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: BTOOKES, A. Anders: REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: 98340P1 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS: LENGTH: 11864 base pairs TYPE: nucleic acid STAPE: acid acid STAPE: double STAPE: double STAPE: Jinear	Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 AGAAATAAGGGGATAAAATATTACCATTTGATGCTAATAACATAAAAGAAGATATGGTA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GITATACAAGGTAATGCAIT---CGCGAGTAGCCATGAAGAAATAGTACGTGCACATCAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408 TATCATTTTATCGGAATTAAGGGATCAGGGATGAGTGCCTTGGCCTTGATGTTGCACCAG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 GAGCAGGCAGGAATTACCATTCTTCCTTTTGATGAAAGAATCTAGACGGTGATATGGAA 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 ATGGGGCACAAGGTTCAGATCAGATGTTGAAAAGTACTACTTTACCCAACGCGGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
30.3%; Score 399.2; DB 4; Length 2
Best Local Similarity 59.1%; Pred. No. 1.4e-83;
Matches 759; Conservative 0; Mismatches 513; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                               APPLICANT: Wallis, Nicola G.
APPLICANT: Black, Michael T.
APPLICANT: Hodgson, John E.
APPLICANT: Knowles, David J.
APPLICANT: Lonetto, Michael A.
APPLICANT: Lonetto, Michael A.
APPLICANT: Stodola, Robert K.
TITLE OF INVENTION: No. 6310193el Murc
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024022
FILING DATE: 16-AUG-1996
APPLICATION NUMBER: US 08/889711
FILING DATE: 08-AUL-1997
ATTORNEY/ACENT INFORMATION:
NAME: Dickinson, Q. Todd
REGISTRATION NUMBER: 28, 354
489 ATCCAAACCTATGAATACTCATTT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER; P50533-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2252
                                                                                                                                              Sequence 1, Application US/08940572
Patent No. 6310193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2715 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215/994-2222
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                                                                                                   RESULT 5
US-08-940-572-1
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1185 AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTT-ATTTA 1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                      531 AATTAATGAAGATTCTATTAATGTATTAGAACAATTGATAATGCTGTTATTTTCATTTA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 TGGGTGCAGGTGATATTCAAAATTACAAATGCATATTTAGATAAATTAGGCATGAAAA 412
                                                                                                                                             651 CAGAAAGITTAAGIAAAGCAGATCGTGTATTTCTTATTGTGAAATTTTTGGATCAATTAG
                                                                      1067 CAGAAAGTTTAAGTAAAGCAGATCGTGTATT--CTTATGTGAAATTTTTGGATCAATTAG
                                                                                                                                                                                                                 1125 AGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAAATTGAAGTGCATCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Lee, Ving J.
APPLICANT: Martin, Partick K.
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
APPLICANT: Sun, Dongxu
ITILE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
ITILE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
ITILE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION NUMBER: 08/14,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STARE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 35° Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERBUCET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 488-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 61, Application US/09265315
Patent No. 6187541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (213) 489-16(
TELEFAX: (213) 955-0440
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US-09-265-315-61/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             771 TCCAAGAANTTAGTGCNNCAATTGAAACCGCACGAAAGAAATATCCACATAAAGAAGT 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    888 TTTAGAGAAGTTAGATG-TCCCAATNTTAAAGAAGCATTAGAAACG-TTGGTGGNGTTAA 831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830 ACGTC-NNTCNATGANACTACAATCGCAAATCAAGTTAATGTAGCTGATTATGNACACCA 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                 APPLICANT: Benton, Bret
APPLICANT: Benton, Wing
APPLICANT: Malouin, Francois
APPLICANT: Malouin, Francois
APPLICANT: Martin, Parrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: US.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 888;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEN IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/114,918
FILING DATE: September 13, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: December 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WAIDLUG, RICHARD J.
TELECOMOUTICATION INFORMATION:
TELECOMOUTICATION:
TELECOMOUTICATION INFORMATION:
TELECOMOUTICATION:
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TELECOMOUTICATION:
TELECOMOUTICATION INFORMATION:
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ZIE: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                           Sequence 61, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
                                                                                         US-08-714-918-61/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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RESULT 9
US-09-266-417-61/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGAAAGTTTAAGTAAAGCAGATCGTGTATT--CTTATGTGAAATTTTTGGATCAATTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1125 AGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAAATTGAAGGTGCATCGTT 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTTT-ATTTA 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGTGCAGGTGATATTCAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAA 1303
                                                                                                                                                                                                                                                                                                                                                               831
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                                                                                                                                                                                                                                                                                                                                    888 ACCICCITICAAIGAAACIACAAIIGCAAAICAAGIIAIIGIAGAIGAIIAIGCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   828 TITAGAGAAGCTAGAIGITACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               651 CAGAAAGTTTAAGTAAAGCAGATCGTGTATTTCTTATTGTGAAATTTTTGGATCAATTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             591 AGAAAATACTGGCGCATTAACGAWACAAGATTTAATTGATAAATTGAAGGTGCATCGTT
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                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                             7;
                                                                                                                                                                              29.6%; Score 389.6; DB 3; Length 888; 94.1%; Pred. No. 1.7e-81; ive 1; Mismatches 21; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bellon, Bret
APPLICANT: Bellon, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Prancois
APPLICANT: Malouin, Parrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: MACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE ON TOTAL ON STAPHYLOCOCCUS AUREUS
TITLE ON TOTAL ON TOTAL
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-265-315-61/c
; Sequence 61, Application US/09265315
; Tetent No. 6187541
; GENERAL INFORMATION:
LENGTH: 888 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                           Query Match 29.6
Best Local Similarity 94.1
Matches 462; Conservative
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                                                                                             linear
                                                            STRANDEDNE

TOPOLOGY:
US-09-265-315-61
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AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTT-ATTTA 1243 1244 TGGGTGCAGGTGATATTCAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAA 1303 531 AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTCATTTA 472 471 TGGGTGCAGGTGATATTCAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAA 412 888 ACGICGITICAAIGAAACTACAAIIGCAAAICAAGIIAIIGIAGAIGAIIAIGCACACCA 830 ACGTC-NNTCNATGANACTACAATCGCAAATCAAGTTAATGTAGCTGATTATGTAGCACA 1008 TGTTGCAGTATTTC-AACCACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTC 711 IGTTGCAGTATNTCAAACCACACTTTCTCTAGAACACACGCATTTTTAAATGAATTTG 1067 CAGAAAGTTTAAGTAAAGCAGATCGTGTATT--CTTATGTGAAATTTTTGGATCAATTAG 651 CAGAAAGTTTAAGTAAAGCAGATCGTGTATTTCTTATTGTGAAATTTTTGGATCAATTAG 591 AGAAAATACTGGCGCATTAACGAWACAAGATTTAATTGATAAATTGAAGGTGCATCGTT 828 ITTAGAGGAAGCTAGATGTTACAAATATTAAAGGAAGCATTAGAAACGTTTGGTGGTGTTAA 771 TCCAAGAGAANTTAGTGCNNCAATTGAAACCGCACGAAAGAATATCCACATAAAGAAGT 1125 AGAAAATACTGGGGGATTAACGATACAAGATTTAATTGATAAAATTGAAGGTGCATCGTT 29.6%; Score 389.6; DB 3; Length 888; 94.1%; Pred. No. 1.7e-81; ive 1; Mismatches 21; Indels 7; CLASSIFICATION 1435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/714,918

FILING DATE: September 13, 1996

APPLICATION NUMBER: 60/009,102

FILING DATE: December 22, 1995

APPLICATION NUMBER: 60/003,798

FILING DATE: September 15, 1995

ATTORNEY/AGENT INPORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REGISTRATION NUMBER: 32,327

TELECOMMUNICATION INFORMATION:

TELEFAK: (213) 955-0440

TELEFAK: 67-3510

INFORMATION FOR SEQ ID NO: 61:

FENENT: 67-3510

SEQUENCE CHARACTERISTICS: 5.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999 C. DOS COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 LENGTH: 888 base pairs TYPE: nucleic acid STRANDEDNESS: single Best Local Similarity 94.1 Matches 462; Conservative 1304 ATGCGTTTTAA 1314 ATGCGTTTTAA 401 TOPOLOGY: linear

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831 947 1007

712

1066

652

1124

1184

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1185 AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTT-ATTTA
                                                                                                                                                                                                                                                                                             531 AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTCATTTA
                                                                                          651 CAGAAAGITIAAGIAAAGCAGAICGIGIATTTCTIATTGIGAAATTTTTGGATCAATTAG
                                                                                                                                             1125 AGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAAATTGAAGGTGCATCGTT
                                                                                                                                                                              1244 TGGGTGCRGGTGATATTCAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sun, Dongxu Sun, Dongxu Sun, Dongxu TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,709
FILING DATE: 17-Mar-2000
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-528-708-61/C
; Sequence 61, Application US/09528709
; Patent No. 6630303
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; Lee, Ving
Malouin, Francois
; Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEK: 67-3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 888 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90071-2066
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1304 ATGCGTTTTAA 1314
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Pred. No. 1.7e-81;
1; Mismatches 21; Indels 7;
                                                                                                  APPLICANT: Lea, Ving J.
APPLICANT: Lea, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Malouin, Perrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CALLIOTHIA
COUNTRY: CALLIOTHIA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 8.5° Diskette, 1.44 Mb
MEDIUM TYPE: 8.5° Diskette, 1.44 Mb
MEDIUM TYPE: 8.0° Diskette, 1.44 Mb
MEDIUM TYPE: 8.0° DOS 5.0
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: MARCH 9, 1999
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/003,798
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
TELEBCOMMUNICATION INFORMATION:
Sequence 61, Application US/09266417
Patent No. 6228588
                                                                         Menton, Bret
Lee, Ving J.
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67.3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.6%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 462; Conservative
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Best Local Similarity
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; Sequence 115, Application US/08961083
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US-08-961-083-115
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                                                                                                                                                                                                                                                                    TGTTGCAGTATTTC-AACCACACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTG 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGTGCAGGTGATATTCAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAA 1303
                                                                                                                                                                                                                                                                                                                      CAGAAAGITTAAGTAAAGCAGATCGTGTATT -- CTTATGTGAAATTTTTGGATCAATTAG 1124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGTCGTTTCAATGAAACTACAATTGCAAATCAAGTTATTGTAGATTATGCACACA
                                                                                                                                                                                                                                    771 TCCAAGAANTTAGTGCNNCAATTGAAACCGCACGAAAGAAATATCCACATAAAGAAGT
                                                                                                                                                                                                                                                                                     AGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAATTGAAGGTGCATCGTT
                                                                                                                                                                                                                  651 CAGAAAGTTTAAGTAAAGCAGATCGTGTATTTCTTATTGTGAAATTTTTGGATCAATTTAG
                                                                                                                                                                                                                                                                                                                                                                                               591 AGAAATACTGGCGCATTAACGAWACAAGATTTAATTGATAAATTGAAGGTGCATCGTT
                                                                                           Gaps
                                                                                        7
                                                               DB 4; Length 888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sun, Dongxu Dongxu Sun, Dongxu TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL TARGET GENES
                                                                                        21; Indels
                                                                                                               TTTAGAGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGT
                                                              29.6%; Score 389.6; DB 4 94.1%; Pred. No. 1.7e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Storage COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                        1; Mismatches
          TOPOLOGY: linear;
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-528-709-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-527-745-61/C
; Sequence 61, Application US/09527745
; Patent No. 6638718
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
; Malouin, Francois
; Malouin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
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                                                                                    Matches 462; Conservative
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                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1125 AGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAAATTGAAGGTGCATCGTT
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Pred. No. 1.7e-81;
1; Mismatches 21;
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/527,745
FILING DATE: 17-Mar-2000
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/003,102
FILING DATE: September 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warbling, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 888 base pairs
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.6%;
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Matches 462; Conservative
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockwille
STATE: Maryland
                                                    GATGCATTCCAAGAAATGGCACATAAAGGTAT
                                                                                                                                                                                                                                                                                                   717 AGGTACTGCTTTTGATGTGTATGTGGTGAGTTTTTATGATCACTTCCTGTCCACA
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                                                                                           TATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTA
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COMPUTER REABBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
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US-09-536-784-115
; Sequence 115, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 rchrercriercrearrhackenhaceacricrrehrhearheeachreeachachacha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 ATTGCCTGAAAGTGATTATTTTGGCTTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 Trodeccahrectahritristritisharereakshransasericaetranses 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                  APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 370.2; DB 3; Length
Pred. No. 5.9e-77;
0; Mismatches 498; Indels
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                            Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PB340P2
                                                                                         STREET: Human Genome Science
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.1%;
Best Local Similarity 58.6%;
Matches 721; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1267 base pairs
                                                                            NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: double
                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                     GENERAL INFORMATION:
Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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RESULT 14
US-09-107-532A-3260
US-09-107-532A
Sequence 3260, Application US/09107532A
Patent No. 6583275
GENERAL INPORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION:
TITLE OF INVENTION:
CONTRIBUTE ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION:
CONTRIBUTED AND THERAPBUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTAGTGCTACAATTGAAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGT 1016
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            717 AGGTACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACA
                                                                          661 TGGTTCAACCTTCACCGTTCATTTCCGTGGACAAAACTTGGGGCAATTCCACATTCCAAC
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                                                                                                                                                                                                                                                                                                                            781 ATTTGATTTGAACTTGGTGGGCACTTGAAAACATTTGCCGGTGTTAAACGTCGTTT
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinfello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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STATE: Massachusetts
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Pred. No. 5.9e-77;
0; Mismatches 498; Indels
                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-OCC-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/961,083
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: MICHAEL S. MATKS
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-536-784-115
                                                                                                                                                                                                                                                                                                                                                                                          TELECONDUNICATION INPORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 1267 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.1%;
58.6%;
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Best Local Similarity 58.61
Matches 721; Conservative
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730 GAIGIGIAIGIGGAIGGIGAGITITAIGAICACIICCIGICICCACAAIAIGGIGACCAI 789
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SOFTWARE: FEBLESG TO: Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,572
                                                                                                                                                                               Sequence 3, Application US/08940572;
Sequence 3, Application US/08940572;
Patent No. 6310193;
GENERAL INFORMATION:
APPLICANT: Wallis, Nicola G.
APPLICANT: Black, Michael T.
APPLICANT: Knowles, David J.
APPLICANT: Lonetto, Michael A.
APPLICANT: Micholas, Richard O.
APPLICANT: Stodola, Robert K.
TITLE OF INVENTION: No. 6310193el MurC
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Pair
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PRICR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER: US 60/024022
FILING DATE: 16-AUG-1996
APPLICATION NUMBER: US 08/889711
FILING DATE: 08-JUL-1997
ATTORNEY/AGENT INPORMATION:
NAME: DICKINSON, Q. TOCK
REPERNOE/DOCKET NUMBER: 28,354
REPERNOE/DOCKET NUMBER: P50533-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2252
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ER: P50533-04
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SEQUENCE CHARACTERISTICS:
LENGTH: 1825 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COUNTRY: USA
ZIP: 19103-2793
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
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US-08-940-572-3/c
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Best Local Simi
Matches 607;
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                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...873
SEQUENCE DESCRIPTION: SEQ ID NO: 3260:
                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
          TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEG ID NO: 3260:
SEQUENCE CHARACTERISTICS:
LENGTH: 873 base pairs
TYPE: NUCleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
REFERENCE/DOCKET NUMBER:
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Matches 535, Conservative
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757 GAIGICIAICAIGGGAIGAAITIGIIGGGCACIICACIGIACACAIICGGIAAACAC 816
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                                                                                                                                817 GATATCITAAATGCITIAGGTGTTATTGCAGTAGCTTATGTCGAGAAACTGGATCT 872
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                                                                                  790 ACAGITITAAAIGCAITAGCIGTAAITGCGAITAGITAITIAGAGAAGCTAGAIGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: Dechert, Price & Rhoads
: 4000 Bell Atlantic Tower, 1717 Arch Stre
Philadelphia
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	444 ITITGAGGCATGTGAATATAGACGTCACITITTAAGTTATAAACCTGATTACGCAATTAT 503	504 GACAAATATTGATTTGATCATCCTGATTATTTAAAGATATTAAAGATGTTTTTGATGC 563 			7	741 GGAIGGICAGITITAIGAICACITICCIGICICCACAAIAIGGIGACCAIACAGITITAAA 800 	801 IGCATTAGCIGTAAATTGGGATTAGTAATTTAGAGAAGCTAGAIGTTACAAATATTAAAGA 860 		921 AGTIATIGIAGATIGATIAIGCACACCATCCAAGAGAAATTAGTGCTACAATIGAAACAGC 980 	981 ACGAAAGAADTATCCACATAAAGAAGTIGTTGCAG-TATTTCAACCACACACTTTCTTA 1039 	1040 GAACACAGGCATTTTAAATGAATTTGCAGAAGTTTAAGTAAAGCAGATCGTATTCT 1099 1017 GAACCATTGCCCTGTTGGACGACTTTGCCCATGCTTTAAACCAAGCAGATGCTGTTTATC 958	1100 TATGTGAAATTTTGGATCAATTAGAGAAAATACTGGGGCATTAACGATACAGATT 1156 	1157 TAATTGATAAAATTGAAGGTGCATCGTTAATTAATGAAGATTCTATTAATGATTAG 1213 		1274 ATGCATAT 1281 777 ACTCATT 770	
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                                                6, 2004, 02:47:10 ; Search time 5352 Seconds
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10673.789 Million cell updates/sec
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BD178031 Murc. 4/2
AR194630 Sequence
AR19458 Sequence
AR405068 Sequence
AR411614 Sequence
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Beattie,B., Domagala,M., Houston,S., Kanagarajah,D., Nethery,K.,
Nq.I., Mansoury,K., Mcdonald,M.L., Pinder,B., Viola,C. and
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel purified polypeptides involved by membrane biosynthesis Patent: WO 03025007-A 27 27-MAR-2003; Affinium Pharmaceuticals, Ind. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                            Description
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Staphylococcus aureus
Bacteria, Firmicutes, Bacillales, Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.7%; Score 1314; Diarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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AX742071
AP003134
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AP01314
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Best Local Similarity
Matches 1314; Conserv
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261 300 RESULT 2 AR354274 321 LOCUS BEFINITION ACCESSION	480 AUIDORS AUIDOR, C.H., 501 TITLE Staphylococcuu 501 FEATURES Local 540 Bource 1 561 ORIGIN 600	720 QY 61 741 Db 687 780 QY 121 801	147 GITGCTCTTAGAATAAGGGGATAAA	960 981 009 301 1020 QY 301 1041 Db 927 1080 QY 421	
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PAT 17-AUG-2003 ö ATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC 686 TTGAGGCATGTGAATATAGACGTCACTTTTTAAGT 1106 SCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA 240 CACATGGTAAAACTTCTACAACAGGTTTATTATCA 360 480 AAATATTACCATTTGATGCTAATAACATAAAGAA 180 CACATGGTAAAACTTCTACAACAGGTTTATTATCA 986 CTTCATTTTAATTGGTGATGGCACAGGTATGGGA 420 CAAATATTGATTTCGATCATCCTGATTATTTTAAA 540 TACGTAAAATTGAAGCAGATGTTCCAATTTATTAT 660 ICCAAGAAAIGGCACAIAAIGIIAAAAAAGGIAII 600 ITTATGCTCAAAATATTCAAATTACGGATAAAGGT 720 ATTAAAGGTICTGGCATGAGTICATTAGCACAAAIC 60 rash, S., Dillon, P.J., Fannon, M.R. and TTGAGGCATGTGAATATAGACGTCACTTTTTAAGT 0; Gaps DB 6; Length 2424; ynucleotides and sequences 15-JUL-2003; linear 0; Indels 24 bp DNA IS 6593114. e 1314; Dl d. No. 0; ismatches n" c DNA"

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Qy 481 TATAAACCTGATTACGCAATTACGAAADATTGATTCGATCATCCTGATTATTTAAA 540 Db 502 TATAAACCTGATTACGCAATTACGAAADATTGATTTCGATCATCCTGATTATTTAAA 561 Cy 541 GATATTATACGCAATTATGACATTCCAAGAAATGCCATAATGTTAAAAAAGGTATT 600 Db 562 GATATTAATGATGCATTTCAAGGCATTCCAAGAAATGGCAATAATTAAAAAAAGGTATT 621 Cy 601 ATTGCTTGGGGTGAAGATGAACATCAACTAAAAATTGAAGATATTATTATTA 621 Cy 601 ATTGCTTGGGGTGAAGATGAACATCAACTAAAAATTGAAGAATTATTATTAT 660	661 682 721 742 742 802 804 841 862 901 961	021 CAACCACACACTITCTCTAGAACACACATITTTAAATGAATTTGCAGAAAGTTTAAGT 1080 1042 CAACACACACTTTCTCTAGAACATTTTAAATGAATTTGCAGAAAGTTTAAGT 1101 029 1081 AAAGCACACTTTCTCTAGAACATTTTTAAATGAATTTGCAGAAAGTTTTAAGT 1101 029 1102 AAAGCAGATCGTGATTCTTATGTGAAATTTTTGGATCAATTAGAGAAATACTGGCGCA 1140 1161 1161 16	AP003134/c LOCUS DEFINITION Staphylococcus aureus subsp. aureus N315 genomic DNA, complete ACCESSION VERSION VERSION AP003134.2 GI:14349226 KEYWORDS SOURCE SOURCE ORGANISM Bacteria; Firmicutes; Bacillales; Staphylococcus I AUTHORS Cui,L., Oguchi,A., Aoki,K., Nadgai,Y., Itoh.T., Kanamori,M., Matsumaru,H., Maruyama,A., Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C.,
	RESULT 4 AX742071 LOCUS AX742071 LOCUS ACCESSION Sequence 29 from Patent W003025007. AX742071 SEQUENCE 29 from Patent W003025007. AX742071 SERVINES STAPPIOCOCCUS aureus SCUNCE ORGANISM BACTERIA: Firmicutes; Bacillales; STaphylococcus. AUTHORS Edwards, A., Dharamsi, A., Vedadi, M., Alam, M.Z., Xwrey, D., Beattie, B., Domagala, M., Gouston, S., Kanagarajah, D., Nethery, K., Moj., M. M., Mologia, M. L., Pinder, B., Viola, C. and M. M. L., Pinder, B., Viola, C. and M. J., Mansoury, K., Mcdonald, M.L., Pinder, B., Viola, C. and M. J., Mansoury, K., Mcdonald, M.L., Pinder, B., Viola, C. and M.S., Location/Qualifiers ITTLE Novel purified polypeptides involved in membrane biosynthesis Location/Qualifiers I. 1335 Source //mol_type="genomic DNA" //db_xref="taxon:1280"	Query Match 95.8%; Score 1263; DB 6; Length 1335; Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0; QY 1 ATGACACATTATGATCATTATGAGATTCAGGATTCAGCATATTAGCACAAATC 0 0 0 0; 0	Qy 241 CATCARTTGAAATTAGATGTATATAGATTTTTAGGACAGATATTTTGATCAA 300 Db 262 CATCAATTGAAATTAGATGTTATAATGATTTTTTAGGACAGATTATTGATCAA 321 Oy 301 TATACTTCAGTAGCTGTAGATGTATATTTTTTTTTATTGATCAA 321 Oy 312 TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA 360 Db 322 TATACTTCAGTAAAAAAACTGGTGACACTGGTAAAACTTCTACACAGGTTATTATTATCA 381 Qy 361 CATGTTATGAATGGTGATAAAAAAGACTTCATTTTAATTGGTGATGGGCACAGGTATGGGA 420 Db 382 CATGTTATGAATGATAAAAAAGACTTCATTTTTAATTGGTGATGGGCACAGGTATGGGA 441 Qy 421 TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT 480 Db 442 TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT 501

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Direct Submission
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complement (1001. .1588)
/gene="SA1294"
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/note="ORFID:SA1294"
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complement(1578. .2153)
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                                                                                    290638 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCACCATCCAAGAGAAATT
    TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT
                     290578 GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT
                                                                                                                                                                                                                                                                                                                                            290398 ACIGCTITIGAIGIGIAIGIGGAIGGIGAGITITIAIGAICACTICCIGICICCACAGIAI
                                                                                                                                                                                                                                                                                                                                                                                                     GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAAACGTCTTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289858 CAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 289805
                                                                 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA
                                                                                                                                                                                            ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT
                                                                                                                                                                                                                          290518 ATTGCTTGGGGTGATGATGAACATCTACGTAAATTGAAGCAGATGTTCCAATTTATTAT
                                                                                                                                                                                                                                                                                                                       721 ACTGCTTTTGATGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT
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                                                                                                                               GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT
                                                                                                                                                                                                                                                          TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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LOCUS
DEFINITION
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complement (8318. .9277)
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'db_xref="GI:13701266"
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                                                                                            complement (7597. .7722)
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Matches 1312; Conserv
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/gene="SAV1633"

complement (5654. .6106)

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complement (6118. .8307)
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IVINSVGDMASKKENNEALVKHFEPVIHECSDCOSKLHTNPMRILDCKVDRDKEAIT
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VTMGDQADRYAVKLLNHLRHNGIKADKDYLQRKIKGQMKQADRLGAKFTIVIGDQELE
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complement (8735. .9253)
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                           complement (3058. .4320)
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complement(6118. .8307)
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complement(8735. .9253)
/gene="apt"
                                                                                                     complement (3058.
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/note="SAV1634"
/codon_start=1
/transl_table=11
                                                                                                                                                                                   'note="SAV1631"
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                                                                      'dene="hiss"
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Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I., Cui, J., Osudi, A., Aoki, K., Naga, T., Lian, J., Ito, T., Kanamori, M., Matsumaru, H., Maruyama, A., Murakami, H., Hooyama, A., Murakami, H., Hooyama, R., Kaito, C., Sekimizu, K., Hirakawa, H., Kuhara, S., Goto, S., Yabuzaki, J., Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C., Shiba, T., Hattori, M., Ospakwara, N., Hayashi, H. and Hiramatsu, K., Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology; 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan Technology; 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan Fax:81.298-53-3454, On May 29, 2001 this sequence version replaced gi:13875943.
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DISKTHTDPMAKIIRQKLKKLGIRKGIPVVFSDESPIVIREDVKDIVGDKNAINRKGQ
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BGFPDIETPVLTKSTPEGARDYLVPSRVHDGEFYALPQSPQLFKQLLMISGFDKYYQI
VKCFDDEDLRADRQPFFYQVDIEMSFYPDGEDVMQMGEFALKKVVKRYKYGFBINGAFPR
MTYKRAMRRYGSDKPDTRFEMELIDVSQLGRDMDFKVFKDTVERNGETKAIVAKGAAE
QYTRKDMDALTEFVNIYGAKGLAWVKVVEDGLTGPIGRFPFFTENVETLITLTGAEAGA
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HHPFTSPKEADIAKLGTAPEEAEANAYDIVLNGYELGGGSIRHHDGELQEKMFRVLGF
TKEGAQEQFGFLLDAFKYGAPPHGGIALGLDRLVMLLTNRTNLRDTIAFPKTASATCL
LTNAPGEVSDKQLEELSLRIRH"
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/protein_id="BAB57790.1"
/db_xref="GI:14247400"
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complement (1029, .1130)
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/protein_id="BAB57792.1"
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| protein_id="BABS791.1"
| db_xref="GI:14247401"
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/db_xref="taxon:158878"
complement(42..815)
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/strain="Mu50"
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/gene="SAV1628"
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                                 GATATTAATGATGTTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.8%;
Matches 1312; Conservative
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ENIYAYATOTGONGUEDEKQUISUVKQGTASKSSDENUSSTTRESMPNYSKUDITIK
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SITHNISQNEDKISQVVQMSNVAMEIADKWQNRHYRRGSANYKANNVATDANHSYISR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-MAR-2002) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center, 2Chome 49-10 Nishibara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@mite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8424)
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Staphylococcus aureus subsp. aureus MW2
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YFMNVKGSYIVYEPFVHPETDKYRLVYQQGITTIKNGQNIHYDFYADAYTGEVINIVE
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/transl_table=11
/product="conserved hypothetical_protein"
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                                                                                                                                                                                                                                                                                 endo-1,4-beta-glucanase homolog'
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Pred. No. 0;
0; Mismatches
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complement(11211. .12053)
/gene="MW1690"
/note="ORFID:MW1690"
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                                                                        table=11
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complement(9612. .10688)
/gene="MW1688"
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             /note="ORFID:MW1687
thioredoxin homolog"
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                                                 /codon_start=1
/transl_table=
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Best Local Similarity 99.8%;
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                                              361 CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA
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                                                                                             TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT
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Antisense antibacterial
Patent: MO 0149775-A 23
Avi Biopharma, Inc. (US)
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YKPDYALMINIDFOHPDYFKDINDVFDAFQENAHVVXGGIIAMGDDEHLAKIEADVPI
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EKEALDVYNIKERALEFFEGYKRENETITANQYIYDDYAHHEREISATIETARKYYPHK
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                                                                                                                                                                                                                                                                                                        Submitted (11-NOV-1997) Channing Laboratory, Brigham and Women's Hospital and Harvard Medical School, 181 Longwood Ave, Boston, MA 02115, USA
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product="UDP-N-acetylmuramoyl-L-alanine synthetase"
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/db_xref="GI:2642659"
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                                                                                   Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
Lowe, A.B. and Deresiewicz, R.L.
Cloning and sequencing of Staphylococcus aureus messential for cell wall biosynthesis
DNA Seq. 10 (1), 19-23. (1999)
                                                                                                                                                                                                                                                                                                                                                                           1. .1314
/organism="Staphylococcus aureus"
/mol_type="genomic DNA"
/db_xref="taxon:1280"
1. .1314
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Pred. No. 0;
0; Mismatches 4
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Lowe, A.M. and Deresiewicz, R.L.
Direct Submission
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(murC) gene, complete cds.
AF034076
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PEATURES Location/Qualifiers 1.1314 /Organism=Staphylococcus aureus" /mol_type="unassigned DNA" ORIGIN Query Match Query Match T5.5%; Score 995; DB 6; Length 1314; Best Local Similarity 99.7%; Pred. No. 0; Matches 1195; Conservative 0; Mismatches 4; Indels 0; Gaps 0; QY 1 ATGACACATATATTGTCGGAATTAAAGGTTCATGACTACATAACAAATC 60 Db 1 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGACTTAACCAAAATC 60	241 121 181 181 241 301 361 421 481	TATAAACCTGATTATGACATTATGACAAATATTGATTTCGATGATGATTATTTAAA TATAAACCTGATTATGACAAATATTGATTTCGATCCTGATTATTTTAAA GATATTAATGATGATTATGACAATATGATGATTTCGATCATTATTTTAAA GATATTAATGATGATTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAGGTATT GATATTAATGATGTTTTTTGATGCATTCCAAGAAATTGAAGCAGATGTTCCAATTTATTAT ATTGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT ATTGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGATGATGATGAAGGTTATTATTATTATTATTATTAT	721 ACTGCTTTTGATGTGTATGGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT 780 [

1 (bases 1 to 1351) Wallis, N.G. and Burnham, M.K.

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Gaps

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6; Length 1351; 4; Indels

80

63.9%; Score 842; DB llarity 99.6%; Pred. No. 0; Conservative 0; Mismatches

Similarity

1. .1351
/organism="unidentified"
/mol_type="genomic DNA"
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Location/Qualifiers

9 81 180

201 240 261 300

321

420 441 480 540

561

501

141

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61

22 AIGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC

TTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC

TATACTICAGIAGCIGIAACIGGIGCACAIGGIAAAACTICTACAACAGGITIAITAICA 360 Argeatgatraggacargaggreaaggarggagarargagaactacgrarracagaa GTTGCTCTTAGAAATAAGGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAAA 181 GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA 202 GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA 241 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA 142 GITGCTCTTAGAAATAAGGGGAATAAAATATTACCATTTGGTGCTAATAACATAAAAGAA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA CATGITATGAATGGTGATAAAAGACTTCATTTTAATTGGTGATGGCACAGGTATGGGA TIGCCTGAAAGTGATTATTTCGCTTTTGAGGCAIGTGAATATAGACGTCACTTTTTAAGT TATAAACCTGATTACGCAATTATGACAAATATTCATTCGATCATCCTGATTATTTAAA 502 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTCAAA 82 121 262 301 322 361 382 481 421 442 ò g ò 쉽 δ PAT 16-APR-2003 linear DNA

> DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 11 BD178030 LOCUS

1351 bp

BD178030 Murc. BD178030 BD178030.1 GI:30015294 JP 2002300888-A/1. unidentified unclassified.

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SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM PLC
OS Unidentified
PN 17 2002300888-A/2
PD 15-CT-2002
PF 25-DEC-2001 JP 2001391079
PR 03-UL-1997 US 60/055720
PI NICOLA G WALLIS, MARTIN K R BURNHAM
PL NICOLA G WALLIS, MARTIN K R BURNHAM
PC CL2N15/09, A6LK31/7088, A6LK38/43, A6LK38/55, A6LK45/00, A6LK48/00, PC
A61P1/02, A61P9/00, A61P1/00, A61P13/12, A61P17/00, PC
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0; Mismatches 3
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Wallis, N.G. and Burnham, M.K.R.
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SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM CORP FUBLIC LTD CO
OS Unidentified
BN JP 1999225773-A/2
BN 24-AUG-1999
PN 34-AUG-1999
PP 03-JUL-1998 JP 1998225115
PR 03-JUL-1998 JP 1998225115
PR 03-JUL-1999 JP 199
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CC Strandedness: Double;

CC Topology: Linear;

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           ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT
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RESULT 12 E35614

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AUTHORS TITLE JOURNAL REFERENCE

COMMENT

FEATURES

Length 619;

1. .619 /organism="unknown" /mol_type="unassigned DNA.

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1 (bases 1 to 619)
Black, M. Terence., Hodgson, J. Edward., Knowles, D. Justin. Charles., Reichard, R. Winfield., Nicholas, R.O., Burnham, M. Karl. Russel., Pratt, J.M., Rosenberg, M., Ward, J.M. and Lonetto, M. Arthur. Prokaryotic polymuclectides polypeptides and their uses Patent: US 6348582-A 179 A9-FEB-2002;
Location/Qualifiere
                                                                                                                                                            Query Match 20.9
Best Local Similarity 99.7
Matches 325, Conservative
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             A61P19/02, A61P19/08, A61P21/00, A61P25/00, A61P27/00, A61P29/00,
                        AG1P31/04,
AG1P39/02,AG1P43/00,C07K14/195,C12N1/15,C12N1/19,C12N1/21,
                                                          C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, C12N15/00,
                                                                                                                                                                                                                                                                                         TIGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCAAAAAAGGTGACC
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Pred. No. 5e-217;
0; Mismatches 3; Indels
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                                                                                                           Location/Qualifiers
                                                                                                                                                        1. .660
/organism="unidentified"
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                                                                                                                        1. .660
                                                                            A61K37/48,A61K37/64
MurC
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Best Local Similarity 99.5%;
Matches 584; Conservative (
A61P17/02,
PC A61P19
PC A61P31
PC A61P31
C12N5/10,
PC C12P21
C12N5/00,
PC A61K37
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                                                                                                                                                                                                                                                                                                                                                                                                                  371 AGTGCTACAATTGACACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT 312
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                                                                                                              611 ACTGCTTTTGATGTGTGTGTGTGTTTTTATGATCACTTCCTGTCTCCAATAT
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                                        Gaps
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Benton, B., Lee, V.J., Malguin, F., Martin, P.K., Schmid, M.B. and
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                                        Indels
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   Score 275; DB 6; L
Pred. No. 3.5e-133;
0; Mismatches 1;
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6228588.
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/mol_type="unassigned DNA"
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AR149358
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1. .888
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Methods of screening
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Patent: US 6228588-A
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linear

Sequence 179 from patent US 6348582. AR194630

GI:20241222

AR194630.1 Unknown. Unknown.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

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507 ATTAGAACAATTIGATAATGCTGTTATTTT 478

Search completed: June 6, 2004, 06:04:07 Job time: 5363 Becs